GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 11, 2003, 11:05:10 ; Search time 93 Seconds
(without alignments)
881.793 Million cell updates/sec

Title: US-09-841-741-2
Perfect score: 2093
Sequence: 1 MTSTCTNSTRESNSSHTCMP.....GTEGGTEGKIVPSYDSATFP 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2024	96.7	508	4	Q96P66	Q96p66 homo sapien
2	430.5	20.6	402	13	Q90X46	Q90x46 brachydanio
3	430	20.5	407	4	O75963	O75963 homo sapien
4	376	18.0	425	6	Q9MZU2	Q9mzu2 oryctolagus
5	376	18.0	429	6	Q9MZU3	Q9mzu3 oryctolagus
6	376	18.0	466	4	Q96RE8	Q96re8 homo sapien
7	371.5	17.7	455	4	O60451	O60451 homo sapien
8	366.5	17.5	429	4	Q13729	Q13729 homo sapien
9	366.5	17.5	499	4	Q13675	Q13675 homo sapien
10	358.5	17.1	466	4	Q9UD63	Q9ud63 homo sapien
11	357	17.1	466	6	Q9TSW7	Q9tsw7 sus scrofa
12	343.5	16.4	408	13	Q98998	Q98998 xenopus lae
13	330.5	15.8	349	4	Q9UD67	Q9ud67 homo sapien
14	325	15.5	391	5	O96716	O96716 branchiosto
15	321	15.3	571	6	Q9TTM9	Q9ttm9 sus scrofa
16	320.5	15.3	422	6	Q9N298	Q9n298 pan troglod
17	320.5	15.3	422	6	Q9N297	Q9n297 gorilla gor
18	319	15.2	515	11	Q9DBL0	Q9dbl0 mus musculu
19	315.5	15.1	422	6	Q9N296	Q9n296 pongo pygma
20	315	15.1	518	6	Q9MYI8	Q9myi8 oryctolagus
21	312.5	14.9	559	11	Q9QW71	Q9qw71 rattus sp.
22	306	14.6	447	6	Q8SPH2	Q8sph2 sus scrofa
23	305.5	14.6	419	5	O77254	O77254 boophilus m
24	301.5	14.4	394	5	Q9NHF3	Q9nhf3 aplysia cal
25	301	14.4	508	5	Q9VCZ3	Q9vcz3 drosophila
26	299.5	14.3	394	5	Q9NJS6	Q9njs6 aplysia kur
27	299	14.3	470	11	P97842	P97842 rattus norv
28	288	13.8	445	4	Q9NZR3	Q9nzr3 homo sapien
29	286	13.7	370	4	Q9H1N4	Q9h1n4 homo sapien
30	285	13.6	443	4	Q9UPA9	Q9upa9 homo sapien
31	280.5	13.4	392	13	Q9YHA5	Q9yha5 myxine glut
32	276.5	13.2	354	13	P87496	P87496 xenopus lae
33	276	13.2	430	5	Q19449	Q19449 caenorhabdi
34	273.5	13.1	534	13	O57422	O57422 xenopus lae
35	272.5	13.0	414	6	Q9GK99	Q9gk99 canis famil
36	271.5	13.0	367	13	Q9DG47	Q9dg47 esox lucius
37	270.5	12.9	372	13	P79945	P79945 xenopus lae
38	270	12.9	378	4	Q96KH9	Q96kh9 homo sapien
39	270	12.9	387	4	Q96KI0	Q96ki0 homo sapien
40	269.5	12.9	388	13	Q90WY4	Q90wy4 brachydanio
41	269	12.9	464	5	Q9GQ54	Q9gq54 aedes aegyp
42	269	12.9	474	4	Q96RG8	Q96rg8 homo sapien
43	268.5	12.8	405	11	Q9CRR2	Q9crr2 mus musculu
44	268.5	12.8	414	6	Q9GKA0	Q9gka0 canis famil
45	267.5	12.8	413	4	Q96EC3	Q96ec3 homo sapien

ALIGNMENTS

RESULT 1
Q96P66
ID Q96P66 PRELIMINARY; PRT; 508 AA.
AC Q96P66;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE G protein-coupled receptor (Putative G-protein coupled receptor).
GN GPR101 OR GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor genes.";
RL Gene 275:83-91(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF411115; AAL26486.1; -.
DR EMBL; AB083588; BAB89301.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95BB5 CRC64;

Query Match 96.7%; Score 2024; DB 4; Length 508;
Best Local Similarity 78.1%; Pred. No. 7.6e-179;
Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;

```
Qy      1 MTSTCTNSTPESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
Db      1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy     61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
Db     61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy    121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
Db    121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
Db    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy    241 CVENEDEEGAEKKEEFQDE----------------------------------------- 259
Db    241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300

Qy    260 ------------------------------------------------------------ 259
Db    301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy    260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
Db    361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy    311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
Db    421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy    371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
Db    481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
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RESULT 2
Q90X46
ID   Q90X46   PRELIMINARY;   PRT;   402 AA.
AC   Q90X46;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   SC:bZ20I5.4 (novel protein similar to human G-protein coupled receptor
DE   RE2)
GN   SC:BZ20I5.4.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lloyd D.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
DR   EMBL; AL590146; CAC94897.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   402 AA; 44373 MW; 5FB8875874267F0C CRC64;

  Query Match   20.6%; Score 430.5; DB 13; Length 402;
  Best Local Similarity   27.9%; Pred. No. 1.3e-31;
  Matches 101; Conservative   78; Mismatches 138; Indels   45; Gaps   7;

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Qy      7 NSTPESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQPKPQLLQVT 66
Db      6 NGTAVANSTNGLDDNGLM-------VLESVSIIIIAILACLGNLVIVVTLYKKPYLLTPS 58

Qy     67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFC--TALVSLTHLFAFASVNTIVV 124
Db     59 NKFVFSLTSSNLLLSVLMLPFVVASSVRRDWMFGVVWCNFTALLHL--LVSSSSMLTLGA 116

Qy    125 VSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSM 184
Db    117 IAIDRYYAVLYPMIYPMKITGNRAVLAIVYIWLHSLVGCLPPLFGWSSFEFDRFKWTCTV 176

Qy    185 IWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVEN 244
Db    177 SWHKEISYTAFWVTWCCLLPLVAMLVCYGVIFRVARIKARKVY----------CGSVVVS 226

Qy    245 EDEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPP--------LPRCYQCKAAKVIFIIIF 296
Db    227 QEESSSQNN-----  ---------GRKNSNTSTSSSGSPKSLIYSGSQCKAFITILVVLG 271

Qy    297 SYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQ 356
Db    272 TFLTTWGPYVVVISTEALLGKNSVSPQ-VETLVSWLSFTSAVCHPLIYGLWNKTVRKELL 330

Qy    357 DM 358
Db    331 GM 332
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RESULT 3
O75963
ID   O75963   PRELIMINARY;   PRT;   407 AA.
AC   O75963;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   G-protein coupled receptor RE2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Raming K.;
RT   "Identification of a novel human G-protein coupled receptor.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF091890; AAC61598.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001, 7tm_1, 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   407 AA; 45363 MW; 00078B8EB5BC1F21 CRC64;

  Query Match   20.5%; Score 430; DB 4; Length 407;
  Best Local Similarity   29.8%; Pred. No. 1.5e-31;
  Matches 101; Conservative   67; Mismatches 135; Indels   36; Gaps   9;

```
Qy     31 GIIRSTVLVIFLAASFV--GNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
Db     25 GVIITQFIAIIVITIFVCLGNLVIVVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFV 84

Qy     89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
Db     85 VTSSIFREWIFGVVWCNFSALLYLLISSASMLTLGVIAIDRYYAVLYPMVYPMKITGNRA 144

Qy    149 YLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVIPLIVM 208
Db    145 VMALVYIWLHSLIGCLPPLFGWSSVEFDEFKWMCVAAWHREPGYTAFWQIWCALFPFLVM 204

Qy    209 IACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIPESLPP 268
Db    205 LVCYGFIFRVAR--------VKARKVHCGTVVIVE-EDAQRTGRKNS-----STSTSSSG 250

Qy    269 SRRNS------NSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY-CFLAVLAVW--VDVET 319
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Db    251 SRRNAFQGVVYSAN-------QCKALITILVVLGAFMVTWGPYMVVIASEALWGKSSVSP 303

Qy    320 QVPQWVITIIIWLFFLQCCIHPYVYYGYMHKTIKKEIQDM 358
          :  |      || |     || :|| :||::||:  |
Db    304 SLETWA----TWLSFASAVCHPLIYGLWNKTVRKELLGM 338


RESULT 4
Q9MZU2
ID   Q9MZU2      PRELIMINARY;      PRT;   425 AA.
AC   Q9MZU2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha 1a-adrenoceptor isoform 3.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BREED NEW ZEALAND WHITE;
RX   MEDLINE=20243335; PubMed=10780960;
RA   Suzuki F., Taniguchi T., Takauji R., Murata S., Muramatsu I.;
RT   "Splice isoforms of alpha(1a)-adrenoceptor in rabbit.";
RL   Br. J. Pharmacol. 129:1569-1576(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF157506; AAF80169.1; -.
DR   HSSP; P02699; 1F88.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   425 AA;  47009 MW;  1202C83BF7644CBF CRC64,

  Query Match             18.0%;  Score 376;  DB 6;  Length 425,
  Best Local Similarity   28.1%;  Pred. No. 1.5e-26;
  Matches  102;  Conservative   70;  Mismatches  155;  Indels   36;  Gaps    8;

Qy      7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
          |::  || :|        |:::  |:   :|   :    :|||:: | :     |  ||
Db      7 NASDSSNCTH-----PPAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT 61

Qy     67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
          : :| || | |||  | | |:     .  .|     ||    :.  |   ||:.:: |:|
Db     62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIISLCVIS 121

Qy    127 VDRYLSIIHPLSYPSKMTQRRGLLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
          :|||: . :|| ||. :|||||    |    |  ::: |  |'.|| | | |:   :| :
Db    122 IDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDD-ETICQI-- 178

Qy    187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
          | | : | :    :|| :::| |  |:  |:|:     : |   |  | :| ::
Db    179 NEEPGYVLFSALGSFYVPLTIILAMYCRVYVVAKPESRGLKSGLKTDKSDSEQVTLRIHP 238

Qy    243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
          :|    |     |: |  |   :     |  ||                |||| : |::
Db    239 KNAPAGGSGVASAKNKTHFSVRL-----LKFSREK------------KAAKTLGIVVGC 280

Qy    298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
          :||   |: || :       . . |: |  |: || :|  ||:| :|    :  ||  |:
Db    281 FVLCWLPF-FLVMPIGSFFPDFKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy    358 MLK 360
          :||
Db    340 VLK 342


RESULT 5
Q9MZU3
ID   Q9MZU3      PRELIMINARY;      PRT;   429 AA.
AC   Q9MZU3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha 1a-adrenoceptor isoform 2.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BREED NEW ZEALAND WHITE;
RX   MEDLINE=20243335; PubMed=10780960;
RA   Suzuki F., Taniguchi T., Takauji R., Murata S., Muramatsu I.;
RT   "Splice isoforms of alpha(1a)-adrenoceptor in rabbit.";
RL   Br. J. Pharmacol. 129:1569-1576(2000).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF157505; AAF80168.1; -.
DR   HSSP; P02699; 1F88.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   429 AA;  47463 MW;  F907B487FCE6D83B CRC64;

  Query Match             18.0%;  Score 376;  DB 6;  Length 429;
  Best Local Similarity   28.1%;  Pred. No. 1.6e-26;
  Matches  102;  Conservative   70;  Mismatches  155;  Indels   36;  Gaps    8;

Qy      7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
          |::  || :|        |:::  |:   :|   :    :|||:: | :     |  ||
Db      7 NASDSSNCTH-----PPAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT 61

Qy     67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
          . :| || | |||  | | |:     .  .|     ||    :.  |   ||:.:: |:|
Db     62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIISLCVIS 121

Qy    127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
          .|||: . :|| ||. :|||||    |    |  ::: |  |'.|| | | |:   :| :
Db    122 IDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDD-ETICQI-- 178

Qy    187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
          | | : | :    :|| :::| |  |:  |:|:     : |   |  | :| ::
Db    179 NEEPGYVLFSALGSFYVPLTIILAMYCRVYVVAKPESRGLKSGLKTDKSDSEQVTLRIHP 238

Qy    243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
          :|    |     |: |  |   :     |  ||                |||| : |::
Db    239 KNAPAGGSGVASAKNKTHFSVRL-----LKFSREK------------KAAKTLGIVVGC 280

Qy    298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
          :||   |: || :       . . |: |  |: || :|  ||:| :|    :  ||  |:
Db    281 FVLCWLPF-FLVMPIGSFFPDFKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy    358 MLK 360
          :||
Db    340 VLK 342


RESULT 6
Q96RE8
ID   Q96RE8      PRELIMINARY;      PRT;   466 AA.
AC   Q96RE8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Adrenergic receptor alpha-1a.
GN   ADRA1A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A
RA   Banerjee A.G.N., Aarti A.;
RT   "RT-PCR cloning and sequence analysis of adrenergic receptor subtype-
RT   alpha-1a cDNA from human prostrate cell-line DU-145.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF395806; AAK77197.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DP   Pfam; PF00001; 7tm_1; 1
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DP   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   466 AA;  51431 MW;  876CBFB3E323B7A1 CRC64;

  Query Match             18.0%;  Score 376;  DB 4;  Length 466;
  Best Local Similarity   27.5%;  Pred. No. 1.7e-26;
  Matches  107;  Conservative   73;  Mismatches  171;  Indels   38;  Gaps   10;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
           |   |:||·   |    |···  |·  :|  :   :|||:: | :     |  ||:
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
             :| || | |||  | | |.     |  :|     ||     :  |   ||. : ..|.
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRPGYLLLYGTWIVAILQSTPPLYGWGQAAFDEPNALCSMIWG 187
           |||· · |||  ||: :|||| · |    | ···· |  ||:|| | |   |   :| :
Db     123 DRYIGVSHPLRYPTIVTQRPGLMALLCVWALSLVISIGPLFGWPQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARFQ----HALLYNVKRHSLEVRVKDCVE 243
             | | : | :    :|| ::·  |  :|:|:      : |   |  | :| ::   :
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKPESPGLKSGLKTDKSDSEQVTLPIHPK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
           |   |      |: |  |   :      |  ||              ||||·|::  :
Db     240 NAPAGGSGMASAKTKTHFSVPL--·LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
           ||   |: || :       : :  : |  |: || :|  ||:| :|    :  ||  |::
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEG 382
           |: :  |:::  |        ||     ||
Db     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEG 369


RESULT 7
O60451
ID   O60451      PRELIMINARY;      PRT;   455 AA.
AC   O60451;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha 1A adrenergic receptor isoform 4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PROSTRATE;
RX   MEDLINE=98149668; PubMed=9490024;
RA   Chang D.J., Chang T.K., Yamanishi S.S., Salazar F.H.R., Kosaka A.H.,
RA   Khare R., Bhakta S., Jasper J.R., Shieh I.-S., Lesnick J.D.,
RA   Ford A.P.D.W., Daniels D.V., Clarke D.E., Bach C.T., Chan H.W.;
RT   "Molecular cloning, genomic characterization and expression of novel
RT   human alpha1A-adrenoceptor isoforms.";
RL   FEBS Lett. 422:279-283(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF013261; AAC06138.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   455 AA;  50802 MW;  80C60918FA608B6C CRC64;

  Query Match             17.7%;  Score 371.5;  DB 4;  Length 455;
  Best Local Similarity   26.9%;  Pred. No. 4.3e-26;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
           |   |:||·   |    |:::  |:  :|       :|||:  | :     |  ||
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
             :| || | |||  | | |:     |  :|     ||     ::  |   ||:  : ::|:
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRPGYLLLYGTWIVAILQSTPPLYGWGQAAFDEPNALCSMIWG 187
           |||· · ·|| ||: :|||| · |    | ···· |  ||:|| | |   |   ·| :
Db     123 DRYIGVSYPLRYPTIVTQRPGLMALLCVWALSLVISIGPLFGWPQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARFQ----HALLYNVKRHSLEVRVKDCVE 243
             | | : | :    :|| ::·  |  :|:|:      : |   |  | :| ::   :
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKPESPGLKSGLKTDKSDSEQVTLPIHPK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
           |   |      |: |  |   :      |  ||              ||||·|::  :
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
           ||   |: || :       : :  : |  |: || :|  ||:| :|    :  ||  |::
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
           |: :  |:::  |        ||     ||  :  . .|     ||
Db     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVPIPVGSRETF 385


RESULT 8
Q13729
ID   Q13729      PRELIMINARY;      PRT;   429 AA.
AC   Q13729;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha 1C adrenergic receptor isoform 3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PROSTATE;
RA   Tanaka T.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 424-429 FROM N.A.
RC   TISSUE=PROSTATE;
RX   MEDLINE=95255557; PubMed=7737411;
RA   Hirasawa A., Shibata K., Horie K., Takei Y., Obika K., Tanaka T.,
RA   Muramoto N., Takagaki K., Yano J., Tsujimoto G.;
RT   "Cloning, functional expression and tissue distribution of human alpha
RT   1C-adrenoceptor splice variants.";
RL   FEBS Lett. 363:256-260(1995).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; D32201; BAA06900.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1
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DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   429 AA;  47514 MW;  A77B05C5D60AF69B CRC64;

  Query Match             17.5%;  Score 366.5;  DB 4;  Length 429;
  Best Local Similarity   26.7%;  Pred. No. 1.2e-25;
  Matches  108;  Conservative   76;  Mismatches  182;  Indels   39;  Gaps   10;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKPESPGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPPCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 9
Q13675
ID   Q13675      PRELIMINARY;      PRT;   499 AA.
AC   Q13675;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha 1C adrenergic receptor isoform 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PROSTATE;
RA   Tanaka T.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PROSTATE;
RX   MEDLINE=95255557; PubMed=7737411;
RA   Hirasawa A., Shibata K., Horie K., Takei Y., Obika K., Tanaka T.,
RA   Muramoto N., Takagaki K., Yano J., Tsujimoto G.;
RT   "Cloning, functional expression and tissue distribution of human alpha
RT   1c-adrenoceptor splice variants.";
RL   FEBS Lett. 363:256-260(1995).
RN   [3]
RP   SEQUENCE OF 202-344 FROM N.A.
RX   MEDLINE=95104335; PubMed=7805763;
RA   Diehl N.L., Shreeve S.M.;
RT   "Identification of the alpha 1c-adrenoceptor in rabbit arteries and
RT   the human saphenous vein using the polymerase chain reaction.";
RL   Eur. J. Pharmacol. 268:393-398(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; D32202; BAA06901.1; -.
DR   EMBL; S76001; AAD14205.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   499 AA;  55000 MW;  BA6E802B6192639D CRC64;

  Query Match             17.5%;  Score 366.5;  DB 4;  Length 499;
  Best Local Similarity   26.7%;  Pred. No. 1.4e-25;
  Matches  108;  Conservative   76;  Mismatches  182;  Indels   39;  Gaps   10;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 10
Q9UD63
ID   Q9UD63      PRELIMINARY;      PRT;   466 AA.
AC   Q9UD63;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha adrenergic receptor subtype alpha 1C.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94296402; PubMed=8024574;
RA   Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
RA   Borkowski D., Strader C.D., Bayne M.;
RT   "Cloning, expression and characterization of human alpha adrenergic
RT   receptors alpha 1a, alpha 1b and alpha 1c.";
RL   Biochem. Biophys. Res. Commun. 201:1296-1304(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ   SEQUENCE   466 AA;  51514 MW;  E4FB501531CFD59C CRC64;
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  Query Match             17.1%;  Score 358.5;  DB 4;  Length 466;
  Best Local Similarity   26.4%;  Pred. No. 7e-25;
  Matches  107;  Conservative   76;  Mismatches  183;  Indels   39;  Gaps   10;

Qy        8 STRESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db        5 SGNASDSSNCTQP-PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy       68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db       63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy      128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db      123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy      188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db      180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy      244 NEDEEG      AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db      240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK-------------KAAKTLGIVVGCF 281

Qy      299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db      282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy      359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
Db      341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385
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RESULT 11
Q9TSW7
ID   Q9TSW7      PRELIMINARY;      PRT;   466 AA.
AC   Q9TSW7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha-1A adrenergic receptor
GN   ALPHA-1A.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uhlen S., Wraith A.;
RT   "Characterization of the pig alpha-1A adrenergic receptor.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AJ251727; CAB62570.1; -.
DR   EMBL; AJ251728; CAB62570.1; JOINED.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   466 AA;  51674 MW;  AEC7F648AC5A719C CRC64;

  Query Match             17.1%;  Score 357;  DB 6;  Length 466;
  Best Local Similarity   26.2%;  Pred. No. 9.7e-25;
  Matches  107;  Conservative   74;  Mismatches  174;  Indels   54;  Gaps   10;

Qy        7 NSTRESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
Db        7 NASDSSNCTH---PPRPVNISKAILLGVILGGLIIFGVLGNILVILSVACHRHLHSVT 61

Qy       67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
Db       62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIIS 121

Qy      127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
Db      122 IDRYIGVSYPLRYPTIVTQKRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI-- 178

Qy      187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ--HALLYNVKRHSLEVRVKDCV 242
Db      179 NEEPGYVLFSALGSFYVPLTIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHR 238

Qy      243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIFS 297
Db      239 KNAPVGGSGVTSAKNKTHFSVRL-----LKFSREK      ----KAAKTLGIVVGC 280

Qy      298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
Db      281 FVLCWLPF-FLVMPIGSFFPDFRPSETVFKIAFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy      358 MLKKFFCKEKPPK--------------EDSHPDL---PGTEGGTEGKI 388
Db      340 VLRIQCLRPKQSSPHALGYTLHPTSHALEEQHKDLVRIPVGSGETFYKI 388
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RESULT 12
Q98998
ID   Q98998      PRELIMINARY;      PRT;   408 AA.
AC   Q98998;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   5-HT1A receptor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=97364954; PubMed=9221903;
RA   Marracci S., Cini D., Nardi I.;
RT   "Cloning and developmental expression of 5-HT1A receptor gene in
RT   Xenopus laevis.";
RL   Mol. Brain Res. 47:67-77(1997).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS.
DR   EMBL; Y07901; CAA69208.1; -.
DR   HSSP; P29274; 1MMH.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   408 AA;  45787 MW;  2CB6156F7D53B1B5 CRC64;

  Query Match             16.4%;  Score 343.5;  DB 13;  Length 408;
  Best Local Similarity   25.4%;  Pred. No. 1.5e-23;
  Matches  100;  Conservative   67;  Mismatches  168;  Indels   59;  Gaps    8;

Qy       23 KMPISLAHGIIPSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQ 80
Db       24 RCPVS--YQIIASLFLGRSFSAGIFGNACVIAAIALER--SLQNVANYLIGSLAVTDLMV 79

Qy       81 ISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYP 140
Db       80 SVLVLPMAAQNQVLNKWTLGQVTCDIFISLDVLCCTSSILHLCAIALDRYWAITDPIDYV 139

Qy      141 SKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSF 200
Db      140 NKRTPRRAAVLISITWIVGFSISIPPMLGWRTP--EDRSDPNACRISEDPGYTIYSTFGA 197
```

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Qy    201 IVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEM 260
          ||||·|·  |  :| |||     ·   ||·  :     |:    :  ||·  | |·
Db    198 FYIPLILMLVLYGKIFKAAR--FRIRKTVKKAEKKKVADTCLSVSQQSPKEKQRGAQQEL 255

Qy    261 N-------------------------------------------IPESLPPSRRN--  272
                                                        || |||: :|
Db    256 EEVGGAQAQRCVNGAIRHGEEGAVLEIIEVHHYVNSKCHLHCKPVPPPEQLPPALKNDRA 315

Qy    273 SNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWL 332
          :  :   :    : |  | · ||· ···|   |:  :|::  : :    :|  :  || ||
Db    316 TEAKRKVALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCET-CHMPHLLFDIITWL 374

Qy    333 FFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKE 366
           :    ::| :| | :|  :   : ::|  ||::
Db    375 GYSNSLLNPIIYAYFNKDFQSAFKKIIKCKFCRQ 408


RESULT 13
Q9UD67
ID   Q9UD67      PRELIMINARY;      PRT;   349 AA.
AC   Q9UD67;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Alpha 1C-adrenoceptor, alpha 1C-AR (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94254631; PubMed=8196478;
RA   Faure C., Pimoule C., Vallancien G., Langer S.Z., Graham D.;
RT   "Identification of alpha 1-adrenoceptor subtypes present in the human
RT   prostate.";
RL   Life Sci. 54:1595-1605(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   NON_TER       1       1
FT   NON_TER     349     349
SQ   SEQUENCE   349 AA;  39361 MW;  B4B3C09824EAC734 CRC64;

  Query Match             15.8%;  Score 330.5;  DB 4;  Length 349;
  Best Local Similarity   27.4%;  Pred. No. 2e-22;
  Matches   96;  Conservative   63;  Mismatches  155;  Indels   37;  Gaps    9;

Qy     62 LLQVTNPFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNT 121
          |  ||: :| || | |||  | | |:    |  :|     ||    ::  |   ||:
Db      6 LHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMG 65

Qy    122 IVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNAL 181
          · ::|:|||: · ·|| ||· ·|||| : |   | ::: |  ||:|| | |   |   :
Db     66 LCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETI 124

Qy    182 CSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVR 237
          | :    | | : |  :    ·|| ::: |  |:  |:|:     :  |   |  | :|
Db    125 CQI--NEEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVT 182

Qy    238 VKDCVENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIF 292
          ::   :|    |      |: |  |   :     | ||                ||||  :
Db    183 LRIHRKNAPAGGSGMASAKTKTHFSVPL-----LKFSREK------------KAAKTLG 224

Qy    293 IIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIK 352
          |::  :||   |: || :       : :  :  |: || :|  ||:| :|    :  |
Db    225 IVVGCFVLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFK 283

Qy    353 KEIQDMLKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
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          |  |::|:    : |   : :    ||     ||  :  : :|     ||
Db    284 KAFQNVLPIQCLPPKQSSKHALGYTLHPPSQAVEGQHKDMVPIPVGSRETF 334


RESULT 14
O96716
ID   O96716      PRELIMINARY;      PRT;   391 AA.
AC   O96716;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Dopamine D1/beta receptor.
OS   Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7740;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cardinaud B., Gibert JM., Sugamori K.S., Coudouel S., Guibert B.,
RA   Vincent J.D., Niznik H.B., Vernier P.;
RT   "The amphioxus D1/beta receptor and the emergence of the vertebrate
RT   adrenergic system.";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ005433; CAA06536.1; -.
DR   HSSP; P29274; 1MMH.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   391 AA;  42622 MW;  67A5AD944AFA3FBE CRC64;

  Query Match             15.5%;  Score 325;  DB 5;  Length 391;
  Best Local Similarity   25.8%;  Pred. No. 7.3e-22;
  Matches   96;  Conservative   67;  Mismatches  159;  Indels   50;  Gaps    8;

Qy      2 TSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQ 61
          | |  | |  |  :       :  | |      :   : || :  : :||::: | :    :
Db     10 TETTANLTANSTEASVGSCFAPNPYSAGVQAVLGLITVILILLTVIGNVLVILAVTCHRK 69

Qy     62 LLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNT 121
             :  ||| || :|   ||      | |:     :  :||    :|   ||   | : ||:
Db     70 MRTVTNFFIVSLACADLSVGITVLPFAATNDILGYWPFGG-YCDVWVSFDVLNSTASILN 128

Qy    122 IVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLY-GW-----GQAAF 175
          .||.: ||:|:|  | :| ::||:|   :|:   | :::: |  |:  ||       : |
Db    129 LVVIAFDRFLAITAPFTYHTRMTERTAGILIATVWGISLVVSFLPIQAGWYRDNQSEEAL 188

Qy    176 DERNALCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLE 235
          ·  |  |· || ·|||·| ·    |||·· |    | ·| ||| !        | ··||
Db    189 AIYSDPCLCIFTASTAYTIVSSLISFYIPLLIMLVFYGIIFKAARDQAR-----KINALE 243

Qy    236 VRVKDCVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIII 295
          |:      | |    ||     |                              |||| : ||:
Db    244 GRL------EQENNRGKKISLAKEK-----------------------KAAKTLGIIM 272

Qy    296 FSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEI 355
          ::|   |:  : ::  : |     |    |   : || ::  | :| :|  :        ||
Db    273 GVFILCWLPFFVVNIVNPFCD--RCVQPAVFIALTWLGWINSCFNPIIYAF-----NKEF 325

Qy    356 QDMLKKFFCKEK 367
          : :  |  |  |
Db    326 RKVFVKMICCHK 337


RESULT 15
Q9TTM9
ID   Q9TTM9      PRELIMINARY;      PRT;   571 AA.
AC   Q9TTM9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Alpha-1D adrenergic receptor.
GN   ALPHA-1D.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uhlen S., Wraith A.;
RT   "Characterization of the pig alpha-1D adrenergic receptor.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
DR   EMBL; AJ250492; CAB59347.1; -.
DR   EMBL; AJ250493; CAB59347.1; JOINED
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   571 AA;  60698 MW;  BACFFB5C903972B1 CRC64;

  Query Match             15.3%;  Score 321;  DB 6;  Length 571;
  Best Local Similarity   28.1%;  Pred. No. 2.6e 21;
  Matches   97;  Conservative   56;  Mismatches  160;  Indels   32;  Gaps   10;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
           | |:      |  |:  :  ||::: | :     |  ||| || || | | |||  : | |:
Db      93 AQGVGVGVFLAAFILMAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLPFS 152

Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
             |  ||     ||   .  |   ||      :||||:   | | ||| ||.|:
Db     153 ATMEVLGFWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPSIMTERKA 212

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207
           :|   | |||: |  || || :    |||   | :   |   | : | :    :|: |
Db     213 AAILALLWAVAIVVSVGPLLGWKEPVPPDER--FCGITEEA--GYAVFSSLCSFYLPMAV 268

Qy     208 MIACYSVVFCAAR RQHALLYNVKRHS-------LEVRVKDCVENEDE-EGA---EKKEE 255
           ::  |  |: ||    :|   |||         | :  :      |   ||    |
Db     269 IVVMYCRVYVVARSTTRSLEAGVKREPGKASEVVLRIHCRGSSTGTDPGHGAMRSTKGHT 328

Qy     256 FQDEMNIPESLPPSERNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWV 315
           |:  ...   |  ||                |||| . |:.  :||   |. |.  |   :
Db     329 FPSSLSL-PILKFSREK------------KAAKTLAIVVGVFVLCWFPFFFVLPLGS-L 373

Qy     316 DVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
           : :   |  :| ||    |  |  |    |      |.
Db     374 FPQLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSPEFKRAFLRLLR 418


Search completed: February 11, 2003, 11:10:12
Job time : 96 secs
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 11, 2003, 11:02:40 ; Search time 14 Seconds
(without alignments)
1179.113 Million cell updates/sec

Title: US-09-841-741-2
Perfect score: 2093
Sequence: 1 MTSTCTNSTRESNSSHTCMP.....GTEGGTEGKIVPSYDSATFP 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	376	18.0	466	1	A1AA_RABIT	O02824 oryctolagus
2	371.5	17.7	466	1	A1AA_HUMAN	P35348 homo sapien
3	371	17.7	466	1	A1AA_RAT	P43140 rattus norv
4	368	17.6	466	1	A1AA_MOUSE	P97718 mus musculu
5	366.5	17.5	466	1	A1AA_CAVPO	Q9wu25 cavia porce
6	356.5	17.0	466	1	A1AA_BOVIN	P18130 bos taurus
7	354	16.9	470	1	A1AA_ORYLA	Q91175 oryzias lat
8	349	16.7	423	1	5H1A_FUGRU	O42385 fugu rubrip
9	332.5	15.9	422	1	5H1A_RAT	P19327 rattus norv
10	326.5	15.6	572	1	A1AD_HUMAN	P25100 homo sapien
11	325	15.5	416	1	5H1B_FUGRU	O42384 fugu rubrip
12	323.5	15.5	562	1	A1AD_MOUSE	P97714 mus musculu
13	321.5	15.4	422	1	5H1A_HUMAN	P08908 homo sapien
14	320.5	15.3	421	1	5H1A_MOUSE	Q64264 mus musculu
15	319	15.2	515	1	A1AB_MESAU	P18841 mesocricetu
16	319	15.2	515	1	A1AB_RAT	P15823 rattus norv
17	319	15.2	519	1	A1AB_HUMAN	P35368 homo sapien
18	315	15.1	576	1	A1AD_RABIT	O02666 oryctolagus
19	314.5	15.0	561	1	A1AD_RAT	P23944 rattus norv
20	305.5	14.6	514	1	A1AB_MOUSE	P97717 mus musculu
21	305	14.6	509	1	5HT_LYMST	Q25414 lymnaea sta
22	303	14.5	446	1	5H7_CAVPO	P50407 cavia porce
23	300	14.3	295	1	A1AA_CANFA	O77621 canis famil
24	299.5	14.3	425	1	5H7_XENLA	Q91559 xenopus lae
25	299	14.3	448	1	5H7_RAT	P32305 rattus norv
26	297	14.2	479	1	5H7_HUMAN	P34969 homo sapien
27	296.5	14.2	490	1	ACM4_CHICK	P17200 gallus gall
28	296	14.1	448	1	5H7_MOUSE	P32304 mus musculu
29	285.5	13.6	499	1	OPS1_PATYE	O15973 patinopecte
30	285	13.6	443	1	D2DR_CERAE	P52702 cercopithec
31	285	13.6	443	1	D2DR_HUMAN	P14416 homo sapien
32	284	13.6	318	1	AA3R_HUMAN	P33765 homo sapien
33	281	13.4	388	1	5H4_CAVPO	O70528 cavia porce
34	279.5	13.4	415	1	B2AR_CANFA	P54833 canis famil
35	277.5	13.3	459	1	5H2C_MOUSE	P34968 mus musculu
36	277	13.2	458	1	5H2C_HUMAN	P28335 homo sapien
37	277	13.2	478	1	OPN4_HUMAN	Q9uhm6 homo sapien
38	275	13.1	460	1	5H2C_RAT	P08909 rattus norv
39	274.5	13.1	400	1	B3AR_MOUSE	P25962 mus musculu
40	273.5	13.1	444	1	D2DR_BOVIN	P20288 bos taurus
41	273	13.0	388	1	5H4_MOUSE	P97288 mus musculu
42	273	13.0	479	1	ACM4_MOUSE	P32211 mus musculu
43	272.5	13.0	415	1	B2AR_MACMU	Q28509 macaca mula
44	272.5	13.0	484	1	ACM4_XENLA	P30544 xenopus lae
45	272	13.0	564	1	5HT1_DROME	P20905 drosophila

ALIGNMENTS

RESULT 1
A1AA_RABIT
ID A1AA_RABIT STANDARD; PRT; 466 AA.
AC O02824;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97324192; PubMed=9180361;
RA Miyamoto S., Taniguchi T., Suzuki F., Takita M., Kosaka N., Negoro E.,
RA Okuda T., Kosaka H., Murata S., Nakamura S., Akagi Y., Oshita M.,
RA Watanabe Y., Muramatsu I.;
RT "Cloning, functional expression and tissue distribution of rabbit
RT alphala-adrenoceptor.";
RL Life Sci. 60:2069-2074(1997).
CC -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC AND G(11) PROTEINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: ABUNDANT IN LIVER, VAS DEFERENS, BRAIN, AND
CC AORTA, BUT NOT IN HEART.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC ----------

CC ----------
DR EMBL; U81982; AAB61334.1; -.
DR HSSP; P02699; 1F88.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 51 1 (POTENTIAL).
FT DOMAIN 52 63 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 64 89 2 (POTENTIAL).
FT DOMAIN 90 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 122 3 (POTENTIAL).
FT DOMAIN 123 143 CYTOPLASMIC (POTENTIAL).

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FT   TRANSMEM     144     168       4 (POTENTIAL).
FT   DOMAIN       169     181       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     182     205       5 (POTENTIAL).
FT   DOMAIN       206     272       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     273     297       6 (POTENTIAL).
FT   DOMAIN       298     304       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     305     329       7 (POTENTIAL).
FT   DOMAIN       330     466       CYTOPLASMIC (POTENTIAL).
FT   LIPID        345     345       PALMITATE (POTENTIAL).
FT   CARBOHYD       7       7       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      13      13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      22      22       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   466 AA;  51365 MW;  9446D356B50FCDE0 CRC64;

  Query Match             18.0%;  Score 376;  DB 1;  Length 466;
  Best Local Similarity   28.1%;  Pred. No. 5.1e-17;
  Matches  102;  Conservative   70;  Mismatches  155;  Indels   36;  Gaps    8;

Qy       7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
           |::  || :|        |:::: |:  :|   :    :|||:: | :      |  ||
Db       7 NASDSSNCTH-----PPAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT 61

Qy      67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
           : :| || | |||  | | |:     :  :|     ||    ::  |   ||: :: |:|
Db      62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIISLCVIS 121

Qy     127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
           :|||: : :|| ||: :|||||   |   |  ::: |  ||:|| | | |:   :| :
Db     122 IDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDD-ETICQI-- 178

Qy     187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
           | | : | :    :|| :::| |  |:  |:|:     : |   |  | :| ::
Db     179 NEEPGYVLFSALGSFYVPLTIILAMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHR 238

Qy     243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
           :|    |     |: |  |   :    | ||               |||| : |::
Db     239 KNAPAGGSGVASAKNKTHFSVRL-----LKFSREK----------KAAKTLGIVVGC 280

Qy     298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
           :||   |: || :       : : |: |  |: || :|  ||:| :|    :  ||  |:
Db     281 FVLCWLPF-FLVMPIGSFFPDFKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy     358 MLK 360
           :||
Db     340 VLK 342


RESULT 2
A1AA_HUMAN
ID   A1AA_HUMAN     STANDARD;      PRT;   466 AA.
AC   P35348;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE   adrenergic receptor).
GN   ADRA1A OR ADRA1C.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
PX   MEDLINE=93384619; PubMed=8396931;
RA   Hirasawa A., Horie K., Tanaka T., Takagaki K., Murai M., Yano J.,
RA   Tsujimoto G.;
RT   "Cloning, functional expression and tissue distribution of human cDNA
RT   for the alpha 1C-adrenergic receptor.";
RL   Biochem. Biophys. Res. Commun. 195:902-909(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Tseng-Crank J.C., Goetz A., Saussy D., Roberson K.M., Hazum S.,
RA   Haizlip J., Godinot N., Wisely B., Robertson C.N., Kost T.;
RL   Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes, and Hippocampus;
RX   MEDLINE=94239386; PubMed=8183249;
RA   Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R.,
RA   Lepor H., Hartig P.R., Weinshank R.L., Branchek T.A.,
RA   Gluchowski C.;
RT   "The alpha 1-adrenergic receptor that mediates smooth muscle
RT   contraction in human prostate has the pharmacological properties of
RT   the cloned human alpha 1c subtype.";
RL   Mol. Pharmacol. 45:703-708(1994).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95114877; PubMed=7815325;
RA   Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA   Worman N.P., Campbell S., Fidock M.D., Furness L.M.,
RA   Parry-Smith D.J., Peter B., Bailey D.S.;
RT   "Cloning and pharmacological characterization of human alpha-1
RT   adrenergic receptors: sequence corrections and direct comparison with
RT   other species homologues.";
RL   J. Pharmacol. Exp. Ther. 272:134-142(1995).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC       ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC       AND G(11) PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: HEART, BRAIN, LIVER AND PROSTATE, BUT NOT IN
CC       KIDNEY, LUNG, ADRENAL, AORTA AND PITUITARY.
CC   -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED
CC       (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D25235; BAA04960.1; -.
DR   EMBL; U02569; AAA93114.1; -.
DR   EMBL; U03866; AAB60353.1; -.
DR   EMBL; L31774; AAB59486.1; -.
DR   Genew; HGNC:277; ADRA1A.
DR   MIM; 104221; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN         1      27       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      28      51       1 (POTENTIAL).
FT   DOMAIN        52      64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      65      88       2 (POTENTIAL).
FT   DOMAIN        89      99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     100     122       3 (POTENTIAL).
FT   DOMAIN       123     143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     144     167       4 (POTENTIAL).
FT   DOMAIN       168     181       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     182     205       5 (POTENTIAL).
FT   DOMAIN       206     273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     274     297       6 (POTENTIAL).
FT   DOMAIN       298     305       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     306     329       7 (POTENTIAL).
FT   DOMAIN       330     466       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD       7       7       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      13      13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      22      22       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

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FT   MOD_RES     215    215       PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT   DISULFID     99    176       BY SIMILARITY.
FT   LIPID       345    345       PALMITATE (POTENTIAL).
FT   CONFLICT     43     43       G -> C (IN REF. 2).
FT   CONFLICT    129    129       S -> T (IN REF. 2).
FT   CONFLICT    347    347       C -> R (IN REF. 1 AND 4).
FT   CONFLICT    359    359       T -> P (IN REF. 2).
FT   CONFLICT    431    431       Q -> E (IN REF. 1).
FT   CONFLICT    442    442       S -> C (IN REF. 2).
SQ   SEQUENCE   466 AA;  51486 MW;  1A50487531DECDF0 CRC64;

  Query Match             17.7%;  Score 371.5;  DB 1;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 9.8e-17;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 3
A1AA_RAT
ID   A1AA_RAT       STANDARD;      PRT;   466 AA.
AC   P43140;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE   adrenergic receptor).
GN   ADRA1A OR ADRA1C.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Heart muscle;
RX   MEDLINE=95008062; PubMed=7923624;
RA   Stewart A.F., Rokosh D.G., Bailey B.A., Karns L.R., Chang K.C.,
RA   Long C.S., Kariya K., Simpson P.C.;
RT   "Cloning of the rat alpha 1C-adrenergic receptor from cardiac
RT   myocytes. Alpha 1C, alpha 1B, and alpha 1D mRNAs are present in
RT   cardiac myocytes but not in cardiac fibroblasts.";
RL   Circ. Res. 75:796-802(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95021119; PubMed=7935320;
RA   Laz T.M., Forray C., Smith K.E., Bard J.A., Vaysse P.J.,
RA   Branchek T.A., Weinshank R.L.;
RT   "The rat homologue of the bovine alpha 1c-adrenergic receptor shows
RT   the pharmacological properties of the classical alpha 1A subtype.";
RL   Mol. Pharmacol. 46:414-422(1994).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC       ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC       AND G(11) PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED
CC       (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U13368; AAA52103.1; -.
DR   EMBL; U07126; AAA62866.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     27       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     28     51       1 (POTENTIAL).
FT   DOMAIN       52     64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     65     88       2 (POTENTIAL).
FT   DOMAIN       89     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    122       3 (POTENTIAL).
FT   DOMAIN      123    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    167       4 (POTENTIAL).
FT   DOMAIN      168    181       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    182    205       5 (POTENTIAL).
FT   DOMAIN      206    273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    274    297       6 (POTENTIAL).
FT   DOMAIN      298    305       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    306    329       7 (POTENTIAL).
FT   DOMAIN      330    466       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      7      7       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     99    176       BY SIMILARITY.
FT   MOD_RES     215    215       PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT   LIPID       345    345       PALMITATE (POTENTIAL).
FT   CONFLICT     39     39       F -> L (IN REF. 1).
FT   CONFLICT     67     67       N -> G (IN REF. 1).
SQ   SEQUENCE   466 AA;  51597 MW;  4962D3A72E971A36 CRC64;

  Query Match             17.7%;  Score 371;  DB 1;  Length 466;
  Best Local Similarity   26.1%;  Pred. No. 1.1e-16;
  Matches  106;  Conservative   78;  Mismatches  180;  Indels   42;  Gaps   10;

Qy       7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
Db       7 NASEGSNCTH-----PPAPVNISKAILLGVILGGLIIFGVLGNILVILSVACHRHLHSVT 61

Qy      67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
Db      62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIIS 121

Qy     127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
Db     122 IDRYIGVSYPLRYPTIVTQRRGVRALLCVWVLSLVISIGPLFGWRQPA-PEDETICQI-- 178

Qy     187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
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Db    179 NEEPGYVLFSALGSFYVPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHR 238

Qy    243 ENEDEEG   - AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297

Db    239 KNVPAEGGGVSSAKNKTHFSVRL-----LKFSREK-----------KAAKTLGIVVGC 280

Qy    298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357

Db    281 FVLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy    358 MLKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397

Db    340 VLPIQCLPPPQSSKHAIGYTLHPPSQALEGQHPDMVPIPVGSGETF 385


RESULT 4
A1AA_MOUSE
ID   A1AA_MOUSE     STANDARD;      PRT;   466 AA.
AC   P97718; O54913;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE   adrenergic receptor).
GN   ADRA1A OR ADRA1C.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=CD-1; TISSUE=Brain, and Kidney;
RX   MEDLINE=98292316; PubMed=9630362;
RA   Xiao L., Scofield M.A., Jeffries W.B.;
RT   "Molecular cloning, expression and characterization of cDNA encoding a
RT   mouse alpha1a-adrenoceptor.";
RL   Br. J. Pharmacol. 124:213-221(1998).
RN   [2]
RP   SEQUENCE OF 197-280 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96064818; PubMed=7595531;
RA   Alonso-Llamazares A., Zamanillo D., Casanova E., Ovalle S., Calvo P.,
RA   Chinchetru M.A.;
RT   "Molecular cloning of alpha 1d-adrenergic receptor and tissue
RT   distribution of three alpha 1-adrenergic receptor subtypes in
RT   mouse.";
RL   J. Neurochem. 65:2387-2392(1995).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC       ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC       AND G(11) PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED
CC       (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF031431; AAC02658.1; -.
DR   EMBL; S80220; AAB47044.1; ALT_INIT.
DR   MGD; MGI:104773; Adra1a.
DR   InterPro; IPR000276; GPCR_Rhodpsn
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     27       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     28     51       1 (POTENTIAL).
FT   DOMAIN       52     64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     65     88       2 (POTENTIAL).
FT   DOMAIN       89     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    122       3 (POTENTIAL).
FT   DOMAIN      123    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    167       4 (POTENTIAL).
FT   DOMAIN      168    181       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    182    205       5 (POTENTIAL).
FT   DOMAIN      206    273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    274    297       6 (POTENTIAL)
FT   DOMAIN      298    305       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    306    329       7 (POTENTIAL).
FT   DOMAIN      330    466       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      7      7       N-LINKED (GLCNAC. . .) (POTENTIAL)
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     215    215       PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT   DISULFID     99    176       BY SIMILARITY.
FT   LIPID       345    345       PALMITATE (POTENTIAL).
SQ   SEQUENCE   466 AA;  51762 MW;  3649A5A53DBD34DA CRC64;

  Query Match             17.6%;  Score 368;  DB 1;  Length 466;
  Best Local Similarity   27.1%;  Pred. No. 1.6e-16;
  Matches  110;  Conservative   75;  Mismatches  179;  Indels   42;  Gaps   11;

Qy      7 NSTRESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66

Db      7 NASEGSNCTH---PPAQVNISKA--ILLGVILGGLIIPGVLGNILVILSVACHPHLHSVT 61

Qy     67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126

Db     62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIIS 121

Qy    127 VDRYLSIIHPLSYPSKMTQPRGYLLLYGTWIVAILQSTPPLYGWGQAAFDEPNALCSMIW 186

Db    122 IDRYIGVSYPLPYPTIVTQPRGVPALLCVWALSLVISIGPLFGWRQQA-PEDETICQI-- 178

Qy    187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242

Db    179 NEEPGYVLFSALGSFYVPLTIILVMYCRVYVVAKRESPGLKSGLKTDKSDSEQVTLPIHR 238

Qy    243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSPPNSNSNPPLPRCYQCKAAKVIFIIIFS 297

Db    239 KNVPAEGGGVSSAKNKTHFSVRL-----LKFSREK---  --------KAAKTLGIVVGC 280

Qy    298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357

Db    281 FVLCWLPF-FLVMPIGSFFPNFKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy    358 MLKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397

Db    340 VLPIQCLPPPQSSKHAIGYTLHPPSQAVEEQHPGMVRIPVGSGETF 385


RESULT 5
A1AA_CAVPO
ID   A1AA_CAVPO     STANDARD;      PRT;   466 AA.
AC   Q9WU25;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE   adrenergic receptor).
GN   ADRA1A.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=Liver;
PX   MEDLINE=21419075; PubMed=11527538;
RA   Gonzalez-Espinosa C., Romero-Avila M.T., Mora-Rodriguez D.M.,
RA   Gonzalez-Espinosa D., Garcia-Sainz J.A.;
RT   "Molecular cloning and functional expression of the guinea pig
RT   alpha(1a)-adrenoceptor.";
RL   Eur. J. Pharmacol. 426:147-155(2001).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC       ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC       AND G(11) PROTEINS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF108016; AAD22540.2; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     51       1 (POTENTIAL).
FT   DOMAIN       52     63       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     64     89       2 (POTENTIAL).
FT   DOMAIN       90     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    122       3 (POTENTIAL).
FT   DOMAIN      123    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    168       4 (POTENTIAL).
FT   DOMAIN      169    181       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    182    205       5 (POTENTIAL).
FT   DOMAIN      206    272       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    273    297       6 (POTENTIAL).
FT   DOMAIN      298    304       EXTRACELLULAR (POTENTIAL)
FT   TRANSMEM    305    329       7 (POTENTIAL).
FT   DOMAIN      330    466       CYTOPLASMIC (POTENTIAL).
FT   LIPID       345    345       PALMITATE (POTENTIAL).
FT   CARBOHYD      7      7       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   466 AA;  51577 MW;  E0E27E4FF5D3D0CD CRC64;

  Query Match           17.5%;  Score 366.5;  DB 1;  Length 466;
  Best Local Similarity  26.1%;  Pred. No. 2e-16;
  Matches  106;  Conservative   75;  Mismatches  184;  Indels   41;  Gaps   10;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNIPKAILLGVILGVLILFGVPGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMSLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQPRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLRALLCLWALSLVISIGPLFGWRQPA-PQDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ-HALLYNVKRHSLEVRVKDCVENED 246
Db     180 EDPSYVLFSALGSFYVPLAIILVMYCRVYVVAKRESRGLTSGLK------ -- --- -- 223

Qy     247 EFGAEKKEEFQDEMNIPESLPP-------SPPNSN--SNPPLPRCYQCKAAKVIFIIIFS 297
Db     224 ---TDKSDSEQVTLPIHPKNAPLGGSGVASSKNKTHFSVRLLKFSREKKAAKTLGIVVGC 280

Qy     298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
Db     281 FVLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy     358 MLKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
Db     340 VLKIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 6
A1AA_BOVIN
ID   A1AA_BOVIN     STANDARD;      PRT;   466 AA.
AC   P18130;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE   adrenergic receptor).
GN   ADRA1A OR ADRA1C.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia, Eutheria, Cetartiodactyla, Ruminantia; Pecora, Bovoidea,
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=90243698; PubMed=1970822;
RA   Schwinn D.A., Lomasney J.W., Lorenz W., Szklut P.J., Fremeau R.T. Jr.,
RA   Yang-Feng T.L., Caron M.G., Lefkowitz R.J., Cotecchia S.;
RT   "Molecular cloning and expression of the cDNA for a novel alpha 1-
RT   adrenergic receptor subtype.";
RL   J. Biol. Chem. 265:8183-8189(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92087349; PubMed=1966743;
RA   Schwinn D.A., Cotecchia S., Lorenz W., Caron M.G., Lefkowitz R.J.;
RT   "The alpha 1C-adrenergic receptor: a new member in the alpha 1-
RT   adrenergic receptor family.";
RL   Trans. Assoc. Am. Physicians 103:112-118(1990).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC       ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC       AND G(11) PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J05426; AAA30374.1; -.
DR   PIR; A35375; A35375.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     27       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     28     51       1 (POTENTIAL).
FT   DOMAIN       52     64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     65     88       2 (POTENTIAL).
FT   DOMAIN       89     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    122       3 (POTENTIAL).
FT   DOMAIN      123    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    167       4 (POTENTIAL).
```

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FT   DOMAIN      168    181       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    182    205       5 (POTENTIAL).
FT   DOMAIN      206    273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    274    297       6 (POTENTIAL).
FT   DOMAIN      298    305       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    306    329       7 (POTENTIAL).
FT   DOMAIN      330    466       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      7      7       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     215    215       PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT   DISULFID     99    176       BY SIMILARITY.
FT   LIPID       345    345       PALMITATE (POTENTIAL).
SQ   SEQUENCE   466 AA;  51466 MW;  77635153B39E85EC CRC64;

  Query Match              17.0%;  Score 356.5;  DB 1;  Length 466;
  Best Local Similarity    25.5%;  Pred. No. 8.6e-16;
  Matches  108,  Conservative   74,  Mismatches  176,  Indels   65,  Gaps   10;

Qy        7 NSTPESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
Db        7 NASDSSNCTH --   PPPPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT 61

Qy       67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
Db       62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNVWAAVDVLCCTASIMGLCIIS 121

Qy      127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
Db      122 IDRYIGVSYPLRYPTIVTQKRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI-- 178

Qy      187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
Db      179 NEEPGYVLFSALGSFYVPLTIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHR 238

Qy      243 ENEDEEG----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
Db      239 KNAQVGGSGVTSAKNKTHFSVRL----LKFSREK     ----  -KAAKTLGIVVGC 280

Qy      298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
Db      281 FVLCWLPF-FLVMPIGSFFPDFRPSETVFKIAFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy      358 MLKKFFCKEKPPK---------------EDSHPDL--------------PGTEGGTEGKI 388
Db      340 VLRIQCLRRKQSSKHTLGYTLHAPSHVLEGQHKDLVRIPVGSAETFYKISKTDGVCEWKI 399

Qy      389 VPS 391
Db      400 FSS 402
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RESULT 7
A1AA_ORYLA
ID   A1AA_ORYLA     STANDARD;      PRT;   470 AA.
AC   Q91175;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Alpha-1A adrenergic receptor (MAR1).
OS   Oryzias latipes (Medaka fish) (Japanese ricefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX   NCBI_TaxID=8090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96184522; PubMed=8654394;
RA   Yasuoka A., Abe K., Arai S., Emori Y.;
RT   "Molecular cloning and functional expression of the alpha1A-
RT   adrenoceptor of Medaka fish, Oryzias latipes.";
RL   Eur. J. Biochem. 235:501-507(1996).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC       ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D63859; BAA09921.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     27       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     28     51       1 (POTENTIAL).
FT   DOMAIN       52     64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     65     88       2 (POTENTIAL).
FT   DOMAIN       89     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    122       3 (POTENTIAL).
FT   DOMAIN      123    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    167       4 (POTENTIAL).
FT   DOMAIN      168    181       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    182    205       5 (POTENTIAL).
FT   DOMAIN      206    271       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    272    295       6 (POTENTIAL).
FT   DOMAIN      296    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    327       7 (POTENTIAL).
FT   DOMAIN      328    470       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      9      9       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     12     12       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     99    176       BY SIMILARITY.
FT   LIPID       343    343       PALMITATE (POTENTIAL).
FT   DOMAIN      351    354       POLY-HIS.
SQ   SEQUENCE   470 AA;  51925 MW;  D4F7A83033061D4E CRC64;

  Query Match              16.9%;  Score 354;  DB 1;  Length 470;
  Best Local Similarity    28.0%;  Pred. No. 1.2e-15;
  Matches  109;  Conservative   63;  Mismatches  193;  Indels   24;  Gaps   10;

Qy       12 SNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIF 71
Db       11 SNCSHVLAP----ELNTVKAVVLGMVLGIFILFGVIGNILVILSVVCHRHLQTVTYYFIV 66

Qy       72 NLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYL 131
Db       67 NLAVADLLLSSTVLPFSAIFEILDRWVFGRVFCNIWAAVDVLCCTASIMSLCVISVDRYI 126

Qy      132 SIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPS 191
Db      127 GVSYPLRYPAIMTKRRALLAVMLLWVLSVIISIGPLFGWKEPA-PEDETVCKIT--EEPG 183

Qy      192 YTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAE 251
Db      184 YAIFSAVGSFYLPLAIILAMYCRVYVVAQKE-----   -SRGLKEGQKIEKSDSEQVI 233

Qy      252 KKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVL 311
Db      234 LRMH RGNTTVSEDEALRSRTHFALRLLKFSREKKAAKTLGIVVGCFVLCWLP--FFLVL 290

Qy      312 AVWVDVETQVP QWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
Db      291 PIGSIFPAYRPSDTVFKITFWLGYFNSCINPIIYLCSNQEFKKAFQSLL-GVHCLRMTPR 349

Qy      371 EDSHPDLPGTEGGTEG-KIVPSYDSATFP 398
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            |  |   :  |:|  :  | ||   |
Db     350 AHHH-HLSVGQSQTQGHSLTISLDSKGAP 377


RESULT 8
5H1A_FUGRU
ID   5H1A_FUGRU     STANDARD;      PRT;   423 AA.
AC   O42385;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   5-hydroxytryptamine 1A-alpha receptor (5-HT-1A-alpha) (Serotonin
DE   receptor) (5-HT1A-alpha) (F1A).
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97361762; PubMed=9218723;
RA   Yamaguchi F., Brenner S.;
RT   "Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor
RT   genes from the Japanese puffer fish, Fugu rubripes.";
RL   Gene 191:219-223(1997).
CC   -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC       HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC       AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC       THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC       CYCLASE ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X95936; CAA65175.1; -.
DR   HSSP; P29274; 1MMH.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     45       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     46     71       1 (POTENTIAL).
FT   DOMAIN       72     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    107       2 (POTENTIAL).
FT   DOMAIN      108    118       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    119    141       3 (POTENTIAL).
FT   DOMAIN      142    161       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    162    186       4 (POTENTIAL).
FT   DOMAIN      188    200       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    201    226       5 (POTENTIAL).
FT   DOMAIN      227    346       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    347    368       6 (POTENTIAL).
FT   DOMAIN      369    379       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    380    404       7 (POTENTIAL).
FT   DOMAIN      405    423       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    118    196       BY SIMILARITY.
FT   CARBOHYD      9      9       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     12     12       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     30     30       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   423 AA;  47000 MW;  7B1308626B40190F CRC64;
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  Query Match           16.7%;  Score 349;  DB 1;  Length 423;
  Best Local Similarity 27.4%;  Pred. No. 2.3e-15;
  Matches  106;  Conservative   60;  Mismatches  163;  Indels   58;  Gaps   10;

Qy      28 LAHGIIRSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVA 85
           |:: || | |   :  |  ||  :| |: |:|   |  | |  | :| ||||:   ||
Db      42 LSYQIITSLFLGALILCSIFGNSCVVAAIALER--SLQNVANYLIGSLAVTDLMVSVLVL 99

Qy      86 PWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQ 145
           |     |  | |    |   ::|  |   :|:  :  :::||| :|  |: | :| |
Db     100 PMAALYQVLNKWTLGQDICDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKRTP 159

Qy     146 RRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVIPL 205
           ||  :|:  ||::    | ||: || ::| |  |    :|    | ||| |      |||
Db     160 RRAAVLISVTWLIGFSISIPPMLGW-RSAEDRANPDACII-SQDPGYTIYSTFGAFYIPL 217

Qy     206 IVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCV----------ENEDEEGAEKKEE 255
           |:|:  |  :| |||    :   ||:          |:           | |   || |
Db     218 ILMLVLYGRIFKAAR--FRIRKTVKKTEKAKASDMCLTLSPAVFHKRANGDAVSAEWKRG 275

Qy     256 FQDEMNIP-----------ESLPPSRRNSNSNP--PIPRCYQC--------------- 285
           :: : : |            |||     ||||    |||   |
Db     276 YKFKPSSPCANGAVRHGEEMESLEIIEVNSNSKTHLPLPNTPQSSSHENINEKTTGTRRK 335

Qy     286 -------KAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCC 338
                 |  | : ||: :::    |:  :|::  :      :|:|:  :| || :
Db     336 IALARERKTVKTLGIIMGTFIFCWLPFFIVALVLPFCAENCYMPEWLGAVINWLGYSNSL 395

Qy     339 IHPYVYGYMHKTIKKEIQDMLKKFFCK 365
           ::| :| | :|  :   : :|:   ||
Db     396 LNPIIYAYFNKDFQSAFKKILR---CK 419


RESULT 9
5H1A_RAT
ID   5H1A_RAT       STANDARD;      PRT;   422 AA.
AC   P19327;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor) (5-
DE   HT1A).
GN   HTR1A OR 5HT1A.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90202832; PubMed=2156831;
RA   Albert P.R., Zhou Q.-Y., van Tol H.H.M., Bunzow J.R., Civelli O.;
RT   "Cloning, functional expression, and mRNA tissue distribution of the
RT   rat 5-hydroxytryptamine1A receptor gene.";
RL   J. Biol. Chem. 265:5825-5832(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90355775; PubMed=2167416;
RA   Fujiwara Y., Nelson D.L., Kashihara K., Varga E., Roeske W.R.,
RA   Yamamura H.I.;
RT   "Role of cytochrome P450 in the control of the production of
RT   erythropoietin.";
RL   Life Sci. 47:127-132(1990).
CC   -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC       HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC       AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC       THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC       CYCLASE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; J05276; AAA40612.1; -.
DR   PIR; A35181; A35181.
DR   PIR; JH0315; JH0315.
DR   HSSP; P29274; 1MMH.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     36       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     37     62       1 (POTENTIAL).
FT   DOMAIN       63     73       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     74     98       2 (POTENTIAL).
FT   DOMAIN       99    109       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    110    132       3 (POTENTIAL).
FT   DOMAIN      133    152       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    153    178       4 (POTENTIAL).
FT   DOMAIN      179    191       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    192    217       5 (POTENTIAL).
FT   DOMAIN      218    345       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    346    367       6 (POTENTIAL).
FT   DOMAIN      368    378       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    379    403       7 (POTENTIAL).
FT   DOMAIN      404    422       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    109    187       BY SIMILARITY.
FT   CONFLICT    373    373       S -> N (IN REF. 2).
SQ   SEQUENCE   422 AA;  46429 MW;  19C2731834C4BBC9 CRC64;

  Query Match             15.9%;  Score 331.5;  DB 1;  Length 422;
  Best Local Similarity   24.4%;  Pred. No. 2.5e-14;
  Matches   98;  Conservative   69;  Mismatches  163;  Indels   71;  Gaps    8;

Qy         26 ISLAHGIIFSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 83
Db         31 VTFSYQVITSLLLGTLIFCAVLGNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88

Qy         84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
Db         89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148

Qy        144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
Db        149 TPRRAAALISLTWLIGFLISIPPMLGWRTP  EDRSDPDACTISKDHGYTIYSTFGAFYI 206

Qy        204 PLIVMIACYSVVFCAAPPQHALLYNVKPHSLEVRVKD----------------------- 240
Db        207 PLLLMLVLYGRIFRAAR------FRIRKTVRKVEKKGAGTSLGTSSAPPPKKSLNGQPGS 260

Qy        241  -  CVENE             ---DEEGAEKKEEFQDEMNIFESLP PSRRNSNSNPP - 278
Db        261 GDWRRCAENRAVGTPCTNGAVRQGDDEATLEVIEVHRVGNSKEHLPLPSESGSNSYAPAC 320

Qy        279 --------------LPPCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQW 324
Db        321 LERKNERNAEAKRKMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCESSCHMPAL 380

Qy        325 VITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCK 365
Db        381 LGAIINWLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCKFCR 421
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RESULT 10
A1AD_HUMAN
ID   A1AD_HUMAN     STANDARD;      PRT;   572 AA.
AC   P25100;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
DE   adrenergic receptor).
GN   ADRA1D OR ADRA1A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hippocampus;
RX   MEDLINE=92028892; PubMed=1656955;
RA   Bruno J.F., Whittaker J., Song J., Berelowitz M.;
RT   "Molecular cloning and sequencing of a cDNA encoding a human alpha 1A
RT   adrenergic receptor.";
RL   Biochem. Biophys. Res. Commun. 179:1485-1490(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hippocampus;
RX   MEDLINE=94239386; PubMed=8183249;
RA   Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R.,
RA   Lepor H., Hartig P.R., Weinshank R.L., Branchek T.A.,
RA   Gluchowski C.;
RT   "The alpha 1-adrenergic receptor that mediates smooth muscle
RT   contraction in human prostate has the pharmacological properties of
RT   the cloned human alpha 1c subtype.";
RL   Mol. Pharmacol. 45:703-708(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95114877; PubMed=7815325;
RA   Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA   Worman N.P., Campbell S., Fidock M.D., Furness L.M.,
RA   Parry-Smith D.J., Peter B., Bailey D.S.;
RT   "Cloning and pharmacological characterization of human alpha-1
RT   adrenergic receptors: sequence corrections and direct comparison with
RT   other species homologues.";
RL   J. Pharmacol. Exp. Ther. 272:134-142(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94296402; PubMed=8024574;
RA   Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
RA   Borkowski D., Strader C.D., Bayne M.;
RT   "Cloning, expression and characterization of human alpha adrenergic
RT   receptors alpha 1a, alpha 1b and alpha 1c.";
RL   Biochem. Biophys. Res. Commun. 201:1296-1304(1994).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta, and Prostate;
RX   MEDLINE=95265059; PubMed=7746284;
RA   Esbenshade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA   Minneman K.P., Murphy T.J.;
RT   "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT   expression of three human subtypes in SK-N-MC cells.";
RL   Mol. Pharmacol. 47:977-985(1995).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
CC       THROUGH THE INFLUX OF EXTRACELLULAR CALCIUM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -----------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
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DR   EMBL; M76446; AAA35496.1; -.
DR   EMBL; U03864; AAB60351.1; -.
DR   EMBL; L31772; AAB59487.1; -.
DR   EMBL; S70782; AAB31163.2; -.
DR   EMBL; D29952; BAA06222.1; -.
DR   PIR; JH0447; JH0447.
DR   Genew; HGNC:280; ADRA1D.
DR   MIM; 104219; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     95       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     96    121       1 (POTENTIAL).
FT   DOMAIN      122    133       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    134    159       2 (POTENTIAL).
FT   DOMAIN      160    169       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    170    192       3 (POTENTIAL).
FT   DOMAIN      193    213       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    214    238       4 (POTENTIAL).
FT   DOMAIN      239    251       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    252    275       5 (POTENTIAL).
FT   DOMAIN      276    348       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    349    373       6 (POTENTIAL).
FT   DOMAIN      374    380       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    381    405       7 (POTENTIAL).
FT   DOMAIN      406    572       CYTOPLASMIC (POTENTIAL).
FT   LIPID       419    419       PALMITATE (POTENTIAL).
FT   DOMAIN      422    428       POLY-ARG.
FT   CONFLICT      1     83       MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
FT                                PAVGGVPGGAGGGGGVVGAGSGEDNRSSAGEPGSAGAGGD
FT                                VNG -> MAAALRSVMMAGYLSEWRTPTYRSTEMVQRLRM
FT                                EAVQHSTS (IN REF. 1).
FT   CONFLICT     31     31       S -> G (IN REF. 4).
FT   CONFLICT    489    572       KPPSAFREWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQR
FT                                AEAACAQRSEVEAVSLGVPHEVAEGATCQAYELADYSNLR
FT                                ETDI -> SHPAPSASGGCWGRSGDPRPSCAPKSPACRTR
FT                                SPPGARSAQRQRAPSAQRWRLCP (IN REF. 1)
FT   CONFLICT    522    522       P -> P (IN REF. 4).
SQ   SEQUENCE   572 AA;  60462 MW;  EBEB134CF20A4988 CRC64;

  Query Match             15.6%;  Score 326.5;  DB 1;  Length 572;
  Best Local Similarity   27.7%;  Pred. No. 7.9e-14;
  Matches   96;  Conservative   58;  Mismatches  157;  Indels   35;  Gaps   10;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
           | |:    |  |:  :  ||::: | :     |  ||| || || | |||  : | |:
Db      94 AQGVGVGVFLAAFILMAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLPFS 153

Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
             |  ||     ||    ::  |   ||· ·:  :|||||: : | | ||· ||·|·
Db     154 ATMEVLGFWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 213

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207
             :|   |:||:: |  || || :    |||   | :   |   | : | |    :|: |
Db     214 AAILALLWVVALVVSVGPLLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLPMAV 269

Qy     208 MIACYSVVFCAAR-RQHALLYNVKRHS-------LEVRVKDCVENEDEEGAE-----KKE 254
           ::  |  |:  ||    ·|   |||          | :  ·     |  ||       |
Db     270 IVVMYCRVYVVARSTTRSLEAGVKRERGKASEVVLRIHCRGAATGAD--GAHGMRSAKGH 327

Qy     255 EFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVW 314
           |:  :::   |  ||                |||| : |::  :||   |: |:  |
Db     328 TFPSSLSV-PLLKFSPEK------------KAAKTLAIVVGVFVLCWFPFFFVLPLGS- 372

Qy     315 VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
           :  : :  : |  .| || :   |::| :|    :  |:    :|:
Db     373 LFPQLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 418
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RESULT 11
5H1B_FUGRU
ID   5H1B_FUGRU     STANDARD;      PRT;   416 AA.
AC   O42384;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   5-hydroxytryptamine 1A-beta receptor (5-HT-1A-beta) (Serotonin
DE   receptor) (5-HT1A-beta) (F1B).
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97361762; PubMed=9218723;
RA   Yamaguchi F., Brenner S.;
RT   "Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor
RT   genes from the Japanese puffer fish, Fugu rubripes.";
RL   Gene 191:219-223(1997).
CC   -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC       HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC       AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC       THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC       CYCLASE ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
CC       STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X95937; CAA65176.1; -.
DR   HSSP; P29274, 1MMH.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     59       1 (POTENTIAL).
FT   DOMAIN       60     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     95       2 (POTENTIAL).
FT   DOMAIN       96    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    129       3 (POTENTIAL).
FT   DOMAIN      130    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    176       4 (POTENTIAL).
FT   DOMAIN      181    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    194    219       5 (POTENTIAL).
FT   DOMAIN      220    339       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    340    361       6 (POTENTIAL).
FT   DOMAIN      362    372       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    373    397       7 (POTENTIAL).
FT   DOMAIN      398    416       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    106    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     18     18       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   416 AA;  47031 MW;  9B4CC415BEC750FE CRC64;

  Query Match             15.5%;  Score 325;  DB 1;  Length 416;
  Best Local Similarity   25.2%;  Pred. No. 7.4e-14;
  Matches  107;  Conservative   66;  Mismatches  174;  Indels   78;  Gaps   13;
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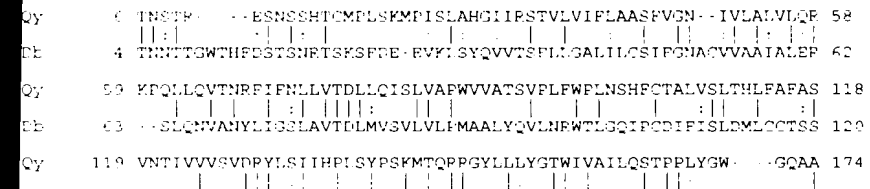

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Qy       6 TNSTP---ESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGN--IVLALVLQR 58
Db       4 TNNTTGWTHFSSTSNRTSKSFDE-EVPLSYQVVTSFLLGALILCSIFGNACVVAAIALEF 62

Qy      59 KPQLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFAS 118
Db      63 --SLQNVANYLIGSLAVTDLMVSVLVLPMAALYQVLNRWTLGQIPCDIFISLDVLCCTSS 120

Qy     119 VNTIVVVSVDRYLSIIHPLSYPSKMTQRPGYLLLYGTWIVAILQSTPPLYGW---GQAA 174
Db     121 ILHLCVIALDRYWAITDPIDYMKKRTPRPAAVLISVTWLVGFSISIPPMLIMRSQPSSMA 180

Qy     175 FDERNA LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHS 233
Db     181 EDRANSRQCFIT  QDPWYTIYSTFGAFYIPLTLMLVLYGRIFKAARRR-- IPPTVRRT 235

Qy     234 LEVRVKD CVENE       DEEGAEKKEEFQDEMNIPESLP  ------------ 267
Db     236 EKRFVSDTCLALSPAMFHPKTPGDAHGKSWKRSVE-----PPPLPNVNGAVKHAGEGESL 290

Qy     268 ---PSRRNSNSNPPLPR-----------------------CYQCKAAKVIFIIIFSYVL 300
Db     291 DIIEVQSNSRCNLPLPNTPGTVPLFENRHFKATETKPKIALARERKTVKTLGIIMGTFIL 350

Qy     301 SLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
Db     351 CWLPFFIVALVMPFCQESCFMPHWLKDVINWLGYSNSLLNPIIYAYFNKDFQSAFKKIIK 410

Qy     361 KFPCK 365
Db     411 CHPCR 415
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RESULT 12
A1AD_MOUSE
ID   A1AD_MOUSE   STANDARD;   PRT;   562 AA.
AC   P97714; Q61619;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
DE   adrenergic receptor).
GN   ADRA1D OR ADRA1A OR GPCR8
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain,
RX   MEDLINE=96064818; PubMed=7595531;
RA   Alonso Llamazares A., Zamanillo D., Casanova E., Ovalle S., Calvo P.,
RA   Chinchetru M.A.;
RT   "Molecular cloning of alpha 1d-adrenergic receptor and tissue
RT   distribution of three alpha 1-adrenergic receptor subtypes in
RT   mouse.";
RL   J. Neurochem. 65:2387-2392(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=10622215;
RA   Arai K., Tanoue A., Goda N., Takeda M., Takahashi K., Tsujimoto G.;
RT   "Characterization of the mouse a1D-adrenergic receptor gene.",
RL   Jpn. J. Pharmacol. 81:271-278(1999).
RN   [3]
RP   SEQUENCE OF 190-350 FROM N.A.
RC   TISSUE=Testis,
RX   MEDLINE=94116980; PubMed=8288218,
RA   Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
RA   Copeland N.G., Jenkins N.A.;
RT   "Identification, chromosomal location, and genome organization of
RT   mammalian G-protein-coupled receptors.";
RL   Genomics 18:175-184(1993).

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CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
CC       THROUGH THE INFLUX OF EXTRACELLULAR CALCIUM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S80044; AAB47042.1; -
DR   EMBL; AB030642; BAA90312.1; -.
DR   EMBL; AB030641; BAA90312.1; JOINED
DR   EMBL; L20333; AAA16854.1; -.
DR   MGD; MGI:106673; Adra1d
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     90       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     91    115       1 (POTENTIAL).
FT   DOMAIN      116    127       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    128    153       2 (POTENTIAL).
FT   DOMAIN      154    163       EXTRACELLULAR (POTENTIAL)
FT   TRANSMEM    164    186       3 (POTENTIAL).
FT   DOMAIN      187    207       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    208    232       4 (POTENTIAL).
FT   DOMAIN      233    245       EXTRACELLULAR (POTENTIAL)
FT   TRANSMEM    246    269       5 (POTENTIAL).
FT   DOMAIN      270    342       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    343    367       6 (POTENTIAL).
FT   DOMAIN      368    374       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    375    399       7 (POTENTIAL).
FT   DOMAIN      400    562       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     60     60       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       413    413       PALMITATE (POTENTIAL).
FT   DOMAIN       21     57       GLY-RICH.
FT   DOMAIN      416    421       POLY-ARG.
FT   CONFLICT    330    330       R -> G (IN REF. 3).
SQ   SEQUENCE   562 AA;  59857 MW;  6CF15515B9F7FA47 CRC64;
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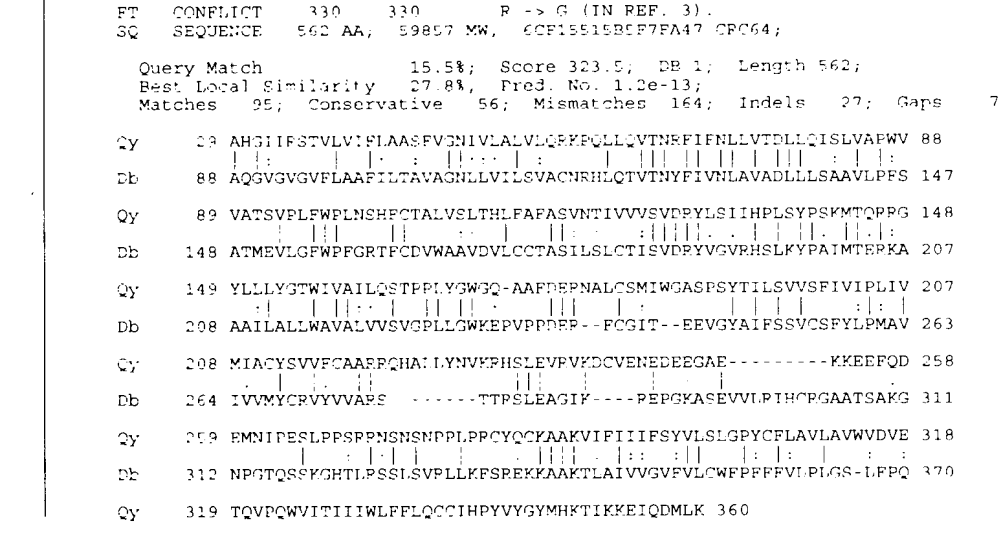
Query Match 15.5%; Score 323.5; DB 1; Length 562;
Best Local Similarity 27.8%; Pred. No. 1.2e-13;
Matches 95; Conservative 56; Mismatches 164; Indels 27; Gaps 7;



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Qy      29 AHGIIPSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
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Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRPG 148
Db     148 ATMEVLGFWPFGRTFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 207

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207
Db     208 AAILALLWAVALVVSVGPLLGWKEPVPPDRP--FCGIT--EEVGYAIFSSVCSFYLPMAV 263

Qy     208 MIACYSVVFCAARRQHALLYNVKRHSLEVPVKDCVENEDEEGAE---------KKEEFQD 258
Db     264 IVVMYCRVYVVARS  ------TTPSLEAGIF----PEPGKASEVVLRIHCPGAATSAKG 311

Qy     259 EMNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVE 318
Db     312 NPGTQSSKGHTLPSSLSVPLLKFSREKKAAKTLAIVVGVFVLCWFPFFFVLPLGS-LFPQ 370

Qy     319 TQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
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Db     371 LKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 412


RESULT 13
5H1A_HUMAN
ID   5H1A_HUMAN      STANDARD;      PRT;   422 AA.
AC   P08908;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor) (5-
DE   HT1A) (G-21).
GN   HTR1A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87315369; PubMed=3041227;
RA   Kobilka B.K., Frielle T., Collins S., Yang-Feng T.L., Kobilka T.S.,
RA   Francke U., Lefkowitz R.J., Caron M.G.;
RT   "An intronless gene encoding a potential member of the family of
RT   receptors coupled to guanine nucleotide regulatory proteins.";
RL   Nature 329:75-79(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Saltzman A.G., Morse B., Felder S.;
RL   Submitted (FEB-1991) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   FUNCTION.
RX   MEDLINE=88334700; PubMed=3138543;
RA   Fargin A., Raymond J.R., Lohse M.L., Kobilka B.K., Caron M.G.,
RA   Lefkowitz R.J.;
RT   "The genomic clone G-21 which resembles a beta-adrenergic receptor
RT   sequence encodes the 5-HT1A receptor.";
RL   Nature 335:358-360(1988).
RN   [4]
RP   VARIANT ASP-272.
RX   MEDLINE=98425601; PubMed=9754630;
RA   Kawanishi Y., Harada S., Tachikawa H., Okubo T., Shiraishi H.;
RT   "Novel mutations in the promoter and coding region of the human 5-HT1A
RT   receptor gene and association analysis in schizophrenia.";
RL   Am. J. Med. Genet. 81:434-439(1998).
CC   -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC       HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC       AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC       THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC       CYCLASE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M28269; AAA36440.1; -.
DR   EMBL; X13556; CAA31908.1; -.
DR   EMBL; X57829; CAA40962.1; -.
DR   EMBL; M83181; AAA66493.1; -.
DR   PIR; S07343; S07343.
DR   PIR; S31438; S31438.
DR   HSSP; P29274; 1MMH.
DR   Genew; HGNC:5286; HTR1A.
DR   MIM; 109760; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Polymorphism.
FT   DOMAIN        1     36       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     37     62       1 (POTENTIAL).
FT   DOMAIN       63     73       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     74     98       2 (POTENTIAL).
FT   DOMAIN       99    109       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    110    132       3 (POTENTIAL).
FT   DOMAIN      133    152       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    153    178       4 (POTENTIAL).
FT   DOMAIN      179    191       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    192    217       5 (POTENTIAL).
FT   DOMAIN      218    345       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    346    367       6 (POTENTIAL).
FT   DOMAIN      368    378       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    379    403       7 (POTENTIAL).
FT   DOMAIN      404    422       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    109    187       BY SIMILARITY.
FT   VARIANT      16     16       P -> L.
FT                                /FTId=VAR_003446.
FT   VARIANT      22     22       G -> S (IN DBSNP:1799920).
FT                                /FTId=VAR_011826.
FT   VARIANT      28     28       I -> V (IN DBSNP:1799921).
FT                                /FTId=VAR_011827.
FT   VARIANT     184    184       P -> L (IN DBSNP:1800043).
FT                                /FTId=VAR_011828.
FT   VARIANT     220    220       R -> L (IN DBSNP:1800044).
FT                                /FTId=VAR_011829.
FT   VARIANT     272    272       G -> D.
FT                                /FTId=VAR_003447.
FT   VARIANT     273    273       G -> D (IN DBSNP:1800042).
FT                                /FTId=VAR_011830.
FT   CONFLICT    152    154       RAA -> PR (IN REF. 1).
FT   CONFLICT    172    172       M -> I (IN REF. 1).
FT   CONFLICT    418    418       K -> N (IN REF. 1).
SQ   SEQUENCE   422 AA;  46106 MW;  762664FCF62CFD8F CRC64;

  Query Match             15.4%;  Score 321.5;  DB 1;  Length 422;
  Best Local Similarity   24.0%;  Pred. No. 1.2e-13;
  Matches   95;  Conservative   72;  Mismatches  170;  Indels   59;  Gaps    7;

Qy      26 ISLAHGIIRSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 83
           ::::: :| | :|    :  : :||  :| |: |:|   |  | | |  | :| ||||:   |
Db      31 VTVSYQVITSLLLGTLIFCAVLGNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88

Qy      84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
           | |      |  | |     |   ::|  |   :|:  :  :::||| :|  |: | :|
Db      89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148

Qy     144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
           | ||   |:  ||::  | | ||: ||     ::|:   :        ||| |      |
Db     149 TPRRAAALISLTWLIGFLISIPPMLGWRTP--EDRSDPDACTISKDHGYTIYSTFGAFYI 206

Qy     204 PLIVMIACYSVVFCAAR-RQHALLYNVKRHSLEVR------------------------ 237
           ||:|:  |  :| ||| |     :  |::   : |
Db     207 PLLLMLVLYGRIFRAARFRIRKTVKKVEKTGADTRHGASPAPQPKKSVNGESGSRNWRLG 266

Qy     238 ----------VKDCVENEDEEGAEKKEEFQDEMNIPESLP-PS----------------R 270
                       |   |:  | :  |      |  | || ||
Db     267 VESKAGGALCANGAVRQGDDGAALEVIEVHRVGNSKEHLPLPSEAGPTPCAPASFERKNE 326

Qy     271 RNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIII 330
           ||: :   :    : |  | : ||: :::|   |:  :|:: : :   :|  :  ||
Db     327 RNAEAKRKMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCESSCHMPTLLGAIIN 386

Qy     331 WLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKE 366
           || :    ::| :| | :|  :   : ::|  ||::
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Db    387 WLGYSNSLLNFVIYAYFNKDFQNAFKKIIKCKFCRQ 422

RESULT 14
5H1A_MOUSE
ID   5H1A_MOUSE     STANDARD;      PRT;   421 AA.
AC   Q64264; Q60956; Q61617;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor) (5-
DE   HT1A).
GN   HTR1A OR GPCR18.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NIH Swiss; TISSUE=Brain;
RX   MEDLINE=94076019; PubMed=8254366;
RA   Charest A., Wainer B.H., Albert P.R.;
RT   "Cloning and differentiation induced expression of a murine
RT   serotonin1A receptor in a septal cell line.";
RL   J. Neurosci. 13:5164-5171(1993).
RN   [2]
RP   SEQUENCE OF 1-23 FROM N.A.
RC   STRAIN=C3H/An;
RX   MEDLINE=96224025; PubMed=8626793;
RA   Parks C.L., Shenk T.;
RT   "The serotonin 1a receptor gene contains a TATA-less promoter that
RT   responds to MAZ and Sp1.";
RL   J. Biol. Chem. 271:4417-4430(1996).
RN   [3]
RP   SEQUENCE OF 130-353 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=94116980; PubMed=8298218;
RA   Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
RA   Copeland N.G., Jenkins N.A.;
RT   "Identification, chromosomal location, and genome organization of
RT   mammalian G-protein-coupled receptors.";
RL   Genomics 18:175-184(1993).
CC   -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC       HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC       AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC       THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC       CYCLASE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MOST ABUNDANTLY EXPRESSED IN MIDBRAIN AND
CC       CORTEX.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U39391; AAA81519.1; -.
DR   EMBL; U33820; AAC52572.1; -.
DR   EMBL; L20339; AAA16850.1; -.
DR   HSSP; P29274; 1MMH.
DR   MGD; MGI:96273; Htr1a.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 2.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family.
FT   DOMAIN        1     36       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     37     62       1 (POTENTIAL).
FT   DOMAIN       63     73       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     74     98       2 (POTENTIAL).
FT   DOMAIN       99    109       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    110    132       3 (POTENTIAL).
FT   DOMAIN      133    152       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    153    178       4 (POTENTIAL).
FT   DOMAIN      179    191       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    192    217       5 (POTENTIAL).
FT   DOMAIN      218    345       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    346    367       6 (POTENTIAL).
FT   DOMAIN      368    378       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    379    403       7 (POTENTIAL).
FT   DOMAIN      404    421       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     10     10       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     11     11       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     30     30       N-LINKED (GLCNAC...) (POTENTIAL).
FT   DISULFID    109    187       BY SIMILARITY.
FT   VARIANT      17     19       EPF -> DHL (IN STRAIN C3H/AN).
FT   CONFLICT    177    177       A -> T (IN REF. 3).
FT   CONFLICT    242    242       F -> L (IN REF. 3).
FT   CONFLICT    247    247       A -> V (IN REF. 3).
FT   CONFLICT    263    263       C -> W (IN REF. 3).
FT   CONFLICT    304    304       D -> H (IN REF. 3).
SQ   SEQUENCE   421 AA;  46123 MW;  CD9513D37A1F499B CRC64;

  Query Match             15.3%;  Score 320.5;  DB 1;  Length 421;
  Best Local Similarity   24.3%;  Pred. No. 1.4e-13;
  Matches   98;  Conservative   74;  Mismatches  155;  Indels   77;  Gaps   12;

Qy         26 ISLAHGIIPSTVLVIFLAASFVGN--IVLALVLQRFPQLLQVTNFFIFNLLVTDLLQISL 83

Db         31 VTFSYQVITSLLLGTLIFCAVLGNAcVVAAIALER-SLQNVANYLIGSLAVTDLMVSVL 88

Qy         84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143

Db         89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148

Qy        144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA-LCSMIWGASPSYTILSVVSFIV 202

Db        149 TPRRAAALISLTWLIGFLISIPPMLGW-RAPEDRSNPNECTI--SKDHGYTIYSTFGAFY 205

Qy        203 IPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVK----------------------- 239

Db        206 IPLLLMLVLYGRIFRAAR------FRIRKTVKKVEKKGAGTSFGTSSAPPPKKSLNGQPG 259

Qy        240 --SCVENEDE---------EGAEKKEEFQDEMNIPE---------SLP-PSRRNSNSNPPL 279

Db        260 SGDCPPSAENRAVGTPCANGAVRQGEDDATLEVIEVHRVGNSKGDLPLPSESGATSY--V 317

Qy        280 PRCY-----------------QCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQV 321

Db        318 PACLRPKNRPTAEAKRKMALAPERKTVKTLGIIMGTFILCWLPFFIVALVLPFCESSCHM 377

Qy        322 PQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCK 365

Db        378 FELLGAIINWLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCKFCP 421


RESULT 15
A1AB_MESAU
ID   A1AB_MESAU     STANDARD;      PRT;   515 AA.
AC   P18841;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor)
GN   ADRA1B.
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89017157; PubMed=2845398;
RA   Cotecchia S., Schwinn D.A., Randall R.R., Lefkowitz R.J.,
RA   Caron M.G., Kobilka B.K.;
RT   "Molecular cloning and expression of the cDNA for the hamster alpha
RT   1-adrenergic receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:7159-7163(1988).
RN   [2]
RP   MUTAGENESIS OF ALA-293.
RX   MEDLINE=92112850; PubMed=1346134;
RA   Kjelsberg M.A., Cotecchia S., Ostrowski J., Caron M.G.,
RA   Lefkowitz R.J.;
RT   "Constitutive activation of the alpha 1B-adrenergic receptor by all
RT   amino acid substitutions at a single site. Evidence for a region
RT   which constrains receptor activation.";
RL   J. Biol. Chem. 267:1430-1433(1992).
CC   -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC       ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J04084; AAA58964.1; -.
DR   PIR; A40491; A40491.
DR   HSSP; P29274; 1MMH.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1     45       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     46     70       1 (POTENTIAL).
FT   DOMAIN       71     83       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     84    105       2 (POTENTIAL).
FT   DOMAIN      106    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    116    141       3 (POTENTIAL).
FT   DOMAIN      142    161       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    162    182       4 (POTENTIAL).
FT   DOMAIN      183    201       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    202    224       5 (POTENTIAL).
FT   DOMAIN      225    295       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    296    319       6 (POTENTIAL).
FT   DOMAIN      320    326       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    327    340       7 (POTENTIAL).
FT   DOMAIN      341    515       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      371    378       POLY-ARG.
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    118    195       BY SIMILARITY.
FT   LIPID       365    365       PALMITATE (POTENTIAL).
FT   MUTAGEN     293    293       A->X: CONFERS CONSTITUTIVE ACTIVITY.
SQ   SEQUENCE   515 AA;  56492 MW;  6DAF1576D1C1CE2D CRC64;

 Query Match             15.2%;  Score 319;  DB 1;  Length 515;
 Best Local Similarity   26.0%;  Pred. No. 2.1e-13;
 Matches   92;  Conservative   70;  Mismatches  162;  Indels   30;  Gaps    7;

Qy      14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
           ||:: :|   :  ::: |:   ||  |:  : ||||:: | :     |   || || ||

Db      32 SSNSTLPQLDVTRAISVGL----VLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87

Qy      74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
             : |||    | |:     |  :| |   ||    ::  |   ||: ::  :|:|||: :
Db      88 AIADLLLSFTVLPFSATLEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147

Qy     134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
           : | ||: :|:|:  | |   |::: : |  || || : | :: :  | :     | |
Db     148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204

Qy     194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL--------YNVKRHSLEVRVKDCVENE 245
           : | :   ||| |::  |  |:  |:|    |         | |  :| :  |:   :|
Db     205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262

Qy     246 DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305
           |   : | :       :|   |   |         ||||  : |::  ::|   |:
Db     263 DTLSSTKAKGHNPRSSIAVKLFKFSREK-----------KAAKTLGIVVGMFILCWLPF 310

Qy     306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDML 359
           |:|:    :    : | |  :: || :   |::| :|    |  |:    :|
Db     311 -FIALPLGSLFSTLKPPDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKRAFMRIL 363


Search completed: February 11, 2003, 11:08:31
Job time : 16 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 11, 2003, 11:02:20 ; Search time 83 Seconds
(without alignments)
638.961 Million cell updates/sec

Title: US-09-841-741-2
Perfect score: 2093
Sequence: 1 MTSTCTNSTRESNSSHTCMP.....GTEGGTEGKIVPSYDSATFP 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2093	100.0	398	23	AAM51646	Human nGPCR-2644 p
2	2024	96.7	508	22	AAU25605	Human G Protein-Co
3	2024	96.7	508	22	AAB86428	Human brain SERALP
4	2024	96.7	508	22	AAU04369	Human G-protein co
5	2024	96.7	508	22	AAG64126	Human G protein-co
6	2024	96.7	508	23	AAU11764	Human alphala adre
7	2024	96.7	926	22	AAU04387	GPCR-Gs fusion pro
8	2021	96.6	508	22	AAB61982	Human G-protein co
9	2021	96.6	508	23	ABB75712	G-protein coupled
10	2019	96.5	508	22	AAU04384	Human G-protein co
11	2002	95.7	508	23	ABB07985	Human seven transm
12	1901	90.8	485	23	AAE15642	Human G-protein co
13	794	37.9	204	22	AAU25561	Human G Protein-Co
14	769.5	36.8	242	23	AAU69568	Human G protein-co
15	430.5	20.6	454	19	AAW58586	Human histamine H2
16	430	20.5	407	21	AAY70343	Human G protein-co
17	422.5	20.2	552	21	AAB14847	Human novel G-prot
18	409	19.5	529	17	AAR90989	Human adrenergic G
19	409	19.5	529	19	AAW70501	Human G-protein ad
20	409	19.5	529	21	AAY57167	Human adrenergic r
21	376	18.0	466	23	ABB09280	G protein-coupled
22	376	18.0	466	23	AAU11765	Alphala adrenergic
23	371.5	17.7	466	15	AAR53073	Alpha 1c adrenergi
24	371.5	17.7	466	15	AAR58680	Human alpha-1C adr
25	371.5	17.7	466	16	AAR90038	Human alpha-1C adr
26	371.5	17.7	466	16	AAR85944	Alpha-1C adrenergi
27	371.5	17.7	466	22	AAU05407	Human adrenorecept
28	371.5	17.7	466	22	AAB59664	Human alpha-1c adr
29	366.5	17.5	429	17	AAW03714	Human alpha-1C3 ad
30	366.5	17.5	466	15	AAR58679	Human alpha-1C adr
31	366.5	17.5	466	16	AAR90037	Human alpha-1C adr
32	366.5	17.5	466	16	AAR73604	Human alpha 1c adr
33	366.5	17.5	466	16	AAR73603	Human alpha 1c adr
34	366.5	17.5	466	21	AAY57170	Sequence of HuAlph
35	366.5	17.5	499	17	AAW03713	Human alpha-1C2 ad
36	365	17.4	375	22	AAU29934	Novel human secret
37	356.5	17.0	466	15	AAR52832	Sequence of human
38	356.5	17.0	466	22	AAB59669	Bovine alpha-1b ad
39	333.5	15.9	375	15	AAR48696	G-protein coupled
40	333.5	15.9	375	17	AAW02668	G-protein coupled
41	329.5	15.7	254	23	ABG66929	G-protein coupled
42	329.5	15.7	254	23	ABB06598	7tm_1,7 transmembr
43	329.5	15.7	254	23	AAU85875	Human GPCR 7tm_1,7
44	329.5	15.7	254	23	AAU85738	Rhodopsin family t
45	326.5	15.6	501	15	AAR70996	Human alpha-1A adr

ALIGNMENTS

RESULT 1
AAM51646
ID AAM51646 standard; Protein; 398 AA.
XX
AC AAM51646;
XX
DT 19-FEB-2002 (first entry)
XX
DE Human nGPCR-2644 polypeptide.
XX
KW Human; G protein-coupled receptor; nGPCR-2644; infection; gene therapy;
KW human immunodeficiency virus; HIV; cancer; diabetes; inflammation;
KW cardiovascular disorder; neurological disorder; rheumatoid arthritis;
KW autoimmune disorder; hormonal disorder; renal failure; psoriasis; asthma.
XX
OS Homo sapiens.
XX
PN WO200181410-A2.
XX
PD 01-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US13249.
XX
PR 25-APR-2000; 2000US-199558P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Lind P, Sejlitz T, Vogeli G;
XX
DR WPI; 2002-041396/05.
DR N-PSDB; ABA03782.
XX
PT Novel G protein-coupled receptor-2644 nucleic acid molecule and

```
PT   polypeptides encoded by them, useful for treating cancers, psoriasis,
PT   Alzheimer's disease, atherosclerosis, rheumatoid arthritis, obesity,
PT   anorexia -
XX
PS   Claim 31; Page 60; 96pp; English.
XX
CC   The invention relates to a gene encoding a novel G protein-coupled
CC   receptor designated nGPCR-2644 nGPCR-2644 polynucleotide and
CC   polypeptides, and antibodies against nGPCR-2644, are useful for
CC   treating diseases such as viral infections caused by human
CC   immunodeficiency virus (HIV)-1 or HIV-2, pain, cancers, diabetes,
CC   obesity, anorexia, hypotension, hypertension, thrombosis, myocardial
CC   infarction, cardiomyopathies, atherosclerosis, Parkinson's disease,
CC   schizophrenia, migraine, anxiety, manic depression, dementia,
CC   Huntington's disease, thyroid disorders, inflammatory conditions,
CC   rheumatoid arthritis, autoimmune disorders, hormonal disorders,
CC   renal failure, psoriasis, movement disorders, asthma and traumatic
CC   brain injury. The present sequence is the nGPCR-2644 polypeptide of
CC   the invention.
XX
SQ   Sequence   398 AA;

  Query Match             100.0%;  Score 2093;  DB 23;  Length 398;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-211;
  Matches  398;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVL 300

Qy     301 SLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 SLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360

Qy     361 KFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           |||||||||||||||||||||||||||||||||||||||
Db     361 KFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 398


RESULT 2
AAU25605
ID   AAU25605 standard; Protein; 508 AA.
XX
AC   AAU25605;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human G Protein-Coupled Receptor (GPCR) polypeptide #52.
XX
KW   Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
KW   attention deficit disorder; anxiety; depression; bipolar disorder;
KW   neurological disorder; Huntington's disease; dementia; obesity; anorexia;
KW   metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
KW   type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
KW   cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
KW   viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;
KW   antidepressant; anorectic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200162797 A2.
XX
PD   30-AUG-2001.
XX
PF   23-FEB-2001; 2001WO-US05676.
XX
PR   23-FEB-2000; 2000US-0184247.
PR   23-FEB-2000; 2000US-0184303.
PR   23-FEB-2000; 2000US-0184304.
PR   23-FEB-2000; 2000US-0184305.
PR   23-FEB-2000; 2000US-0184397.
PR   02-MAR-2000; 2000US-0186457.
PR   03-MAR-2000; 2000US-0186810.
PR   09-MAR-2000; 2000US-0188064.
PR   13-MAR-2000; 2000US-0188880.
PR   03-APR-2000; 2000US-0194344.
PR   23-JUN-2000; 2000US-0213861.
PR   11-JUL-2000; 2000US-0217369.
PR   11-JUL-2000; 2000US-0217370.
PR   14-JUL-2000; 2000US-0218337.
PR   20-JUL-2000; 2000US-0218492.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Vogeli G,  Wood LS,  Parodi LA,  Lind P;
XX
DR   WPI; 2001-570628/64.
DR   N-PSDB; AAS42857.
XX
PT   New isolated nucleic acid encoding a new G-protein coupled receptor
PT   polypeptide for detecting receptor modulators that can treat mental
PT   disorders, such as schizophrenia, anxiety, depression, or obesity -
XX
PS   Claim 35; Page 90; 279pp; English.
XX
CC   Sequences AAU25554-AAU25616 represent human G-protein coupled receptor
CC   (GPCR) polypeptides of the invention. The proteins and their associated
CC   DNA sequences can be used to identify compounds which bind to GPCR
CC   polypeptides and in screening for compounds that modulate GPCR activity.
CC   By screening a human subject for the presence of mutations in GPCR DNA, a
CC   GPCR-related disorder or a genetic predisposition can be diagnosed. The
CC   sequences can also be used for treatment and prevention of mental
CC   disorders such as schizophrenia, attention deficit disorder, anxiety,
CC   depression, dementia and bipolar disorder, neurological disorders such as
CC   Huntington's disease, Parkinson's disease and Tourette's syndrome,
CC   metabolic disorders such as obesity, anorexia and type 2 diabetes,
CC   cardiovascular disorders such as thrombosis, myocardial infarction,
CC   cardiomyopathy and atherosclerosis, viral infections caused by HIV and
CC   cancers.
XX
SQ   Sequence   508 AA;

  Query Match             96.7%;  Score 2024;  DB 22;  Length 508;
  Best Local Similarity   78.1%;  Pred. No. 3.8e-204;
  Matches  397;  Conservative    1;  Mismatches    0;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy    241 CVENEDEEGAEKKEEFQDE---------------------------------------- 259
          |||||||||||||||||||
Db    241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300

Qy    260 ------------------------------------------------------------ 259

Db    301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy    260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                  :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy    311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy    371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
          |||||||||||||||||||||||||||||
Db    481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
```

RESULT 3
AAB86428
ID AAB86428 standard; Protein; 508 AA.
XX
AC AAB86428;
XX
DT 19-OCT-2001 (first entry)
XX
DE Human brain SERALPHA protein.
XX
KW SERALPHA; human; brain; G protein receptor; medicine.
XX
OS Homo sapiens.
XX
PN DE10004930-A1.
XX
PD 09-AUG-2001.
XX
PF 04-FEB-2000; 2000DE-1004930.
XX
PR 04-FEB-2000; 2000DE-1004930.
XX
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
XX
PI Bruess M, Boenisch H;
XX
DR WPI; 2001-489887/54.
DR N-PSDB; AAH48673.
XX
PT Gene encoding a protein of the G protein receptor super family, having
PT homology to neurotransmitter receptors is useful to develop new
PT medicaments -
XX
PS Disclosure; Page 4; 8pp; German.
XX
CC This invention describes a novel human brain-derived G protein receptor
CC gene and its encoding protein, designated SERALPHA. The receptor or cells
CC expressing the receptor are used to develop new medicines, chemicals and
CC technologies, and to devaluate existing medicines and technologies.
XX
SQ Sequence 508 AA;

Query Match 96.7%; Score 2024; DB 22; Length 508;
Best Local Similarity 78.1%; Pred. No. 3.8e-204;
Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;

```
Qy      1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy     61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy    121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy    241 CVENEDEEGAEKKEEFQDE---------------------------------------- 259
          |||||||||||||||||||
Db    241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300

Qy    260 ------------------------------------------------------------ 259

Db    301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy    260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                  :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy    311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy    371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
          |||||||||||||||||||||||||||||
Db    481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
```

RESULT 4
AAU04369
ID AAU04369 standard; Protein; 508 AA.
XX
AC AAU04369;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human G-protein coupled receptor, hRUP15.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP15; agonist;
KW inverse agonist; lung cancer.
XX
OS Homo sapiens.
XX
PN WO200136471-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US31509.
XX
PR 17-NOV-1999; 99US-0166088.
PR 17-NOV-1999; 99US-0166099.
PR 17-NOV-1999; 99US-0166369.
PR 23-DEC-1999; 99US-0171900.
PR 23-DEC-1999; 99US-0171901.
PR 23-DEC-1999; 99US-0171902.
PR 11-FEB-2000; 2000US-0181749.
PR 14-MAR-2000; 2000US-0189258.
PR 14-MAR-2000; 2000US-0189259.
PR 10-APR-2000; 2000US-0195898.
PR 10-APR-2000; 2000US-0195899.
PR 10-APR-2000; 2000US-0196078.
PR 28-APR-2000; 2000US-0200419.
PR 12-MAY-2000; 2000US-0203630.
PR 12-JUN-2000; 2000US-0210741.
PR 12-JUN-2000; 2000US-0210982.
PR 21-AUG-2000; 2000US-0226760.
PR 26-SEP-2000; 2000US-0235418.

```
PR   26-SEP-2000; 2000US-0235779.
PR   20-OCT-2000; 2000US-0242332.
PR   20-OCT-2000; 2000US-0242343.
XX
PA   (APEN-) APENA PHAPM INC.
XX
PI   Chen R,  Dang HT,  Lowitz KP;
XX
DR   WPI; 2001-355616/37.
DR   N-PSDB; AAS07942.
XX
PT   Endogenous and non-endogenous versions of human G-protein coupled
PT   receptors for direct identification of candidate compounds as agonists,
PT   inverse agonists or partial agonists for use as therapeutic agents -
XX
PS   Claim 29; Page 102-104; 160pp; English.
XX
CC   The sequence represents a human G-protein coupled receptor (GPCR),
CC   hRUP15. The endogenous and non-endogenous, constitutively activated
CC   versions of human G-protein coupled receptors (GPCR), are useful for
CC   direct identification of candidate compounds as receptor agonists,
CC   inverse agonists or partial agonists having applicability as therapeutic
CC   agents for treating diseases related to GPCR, e.g. lung cancer.
CC   Non-endogenous version of human GPCRs are also utilized in research
CC   settings and in vitro and in vivo system, incorporating GPCRs can be
CC   utilised to elucidate and understand the roles these receptors
CC   play in the human condition, both normal and diseased.
XX
SQ   Sequence   508 AA;

  Query Match             96.7%;  Score 2024;  DB 22;  Length 508;
  Best Local Similarity   78.1%;  Pred. No. 3.8e-204;
  Matches  397;  Conservative    1;  Mismatches    0;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE---------------------------------- -- - 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300

Qy     260 ------------------------------------------------------------ 259

Db     301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy     260  --------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                    :||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 NFSEDDVEAVNIPESLPPSPPNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy     311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy     371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           |||||||||||||||||||||||||||||
Db     481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508


RESULT 5
AAG64126
ID   AAG64126 standard; Protein; 508 AA.
XX
AC   AAG64126;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human G protein-coupled receptor GPRv72.
XX
KW   Human; guanosine triphosphate binding protein-coupled receptor;
KW   G protein-coupled receptor; GPRv8; GPRv12; GPRv16; GPRv21; GPRv40;
KW   GPRv47; GPRv51; GPRv71; GPRv72, cancer, liver cirrhosis,
KW   Alzheimer's disease; cytostatic; hepatotropic; nootropic;
KW   neuroprotective; gene therapy; peptide therapy.
XX
OS   Homo sapiens.
XX
PN   WO200148188-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-JP09408.
XX
PR   28-DEC-1999;   99JP-0375152.
PR   31-MAR-2000; 2000JP-0101339.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Matsumoto S,  Oda T,  Saito Y,  Morikawa N,  Yoshida K,  Suwa M;
PI   Sugiyama T,  Kishimoto T,  Kanzaki K,  Yasuda S,  Inoue Y;
XX
DR   WPI; 2001-425662/45.
DR   N-PSDB; AAH73517.
XX
PT   New DNA encoding guanosine triphosphate binding protein coupled
PT   receptors and their expression products for screening potential
PT   anticancer and nootropic drugs and in diagnosis of these diseases  -
XX
PS   Claim 1; Page 135-138; 170pp; Japanese.
XX
CC   The invention relates to nine human guanosine triphosphate binding
CC   protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,
CC   GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPPv72, and to the
CC   genes encoding them. These genes and proteins and antibodies against
CC   the protein are useful in the treatment, prevention, diagnosis and
CC   investigation of diseases associated with G protein-coupled receptors,
CC   including cancer, cirrhosis of the liver and Alzheimer's disease.
CC   The present sequence is a G protein-coupled receptor of the invention.
XX
SQ   Sequence   508 AA;

  Query Match             96.7%;  Score 2024;  DB 22;  Length 508;
  Best Local Similarity   78.1%;  Pred. No. 3.8e-204;
  Matches  397;  Conservative    1;  Mismatches    0;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE----- -- ---------------------------- - 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300
```

```
Qy    260 ------------------------------------------------------------ 259

Db    301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy    260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                  :|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy    311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy    371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
          |||||||||||||||||||||||||||||
Db    481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
```

RESULT 6
AAU11764
ID AAU11764 standard; Protein; 508 AA.
XX
AC AAU11764;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human alphala adrenergic receptor-like GPCR.
XX
KW Human; alphala adrenergic receptor; G protein-coupled receptor;
KW GPCR; peripheral nervous system disease; central nervous system disease;
KW urinary incontinence; benign prostatic hypertrophy; infection;
KW HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
KW bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia;
KW Huntington's disease; Tourette's syndrome.
XX
OS Homo sapiens
XX
PN WO200188126-A2.
XX
PD 22-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-EP05383.
XX
PR 15-MAY-2000; 2000US-204145P.
PR 04-DEC-2000; 2000US-250505P.
XX
PA (FARB) BAYER AG.
XX
PI Ramakrishnan S;
XX
DR WPI; 2002-106124/14.
DR N-PSDB; AAS18898, AAS18899.
XX
PT New polynucleotide, useful for treating pain, cancer, Parkinson's
PT diseases, obesity, hypertension, asthma, schizophrenia, encodes an
PT alpha (1a) adrenergic receptor-like G-protein coupled receptor (GPCR) -
XX
PS Claim 25; Fig 3; 123pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding an alphala
CC adrenergic receptor-like G-protein coupled receptor (GPCR) polypeptide,
CC the encoded polypeptide, fragments, derivatives and allelic variants.
CC Also include are an expression vector comprising the polynucleotide,
CC a host cell containing the vector, screening for therapeutic agents which
CC decrease or increase the activity of the receptor by binding a test
CC agent to the protein and determining whether the activity is
CC deceased or increased. A modulator of the receptor is useful for treating
CC alphala adrenergic receptor-like GPCR disorder such as peripheral or
CC central nervous system disease, urinary incontinence or benign prostatic
CC hypertrophy. The receptor, polynucleotide or modulator is useful for
CC treating disorders such as bacterial, fungal, protozoan, and viral
CC infections, particularly those caused by HIV (human immunodeficiency
CC virus), pain, cancer, anorexia, bulimia, asthma, Parkinson's diseases,
CC obesity, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcer,
CC allergy, benign prostatic hypertrophy, and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression,
CC delirium, dementia, severe mental retardation, and dyskinesias, such as
CC Huntington's disease and Tourette's syndrome. The polynucleotide is
CC useful in diagnostic assays for detecting diseases and abnormalities or
CC susceptibility to disease and abnormalities related to the presence of
CC mutations in the gene. The protein is useful to identify test compounds
CC which may act as agonists or antagonists, and for raising antibodies
CC which can block the receptor and effectively prevent ligand binding.
CC The present sequence is the alphala adrenergic receptor-like GPCR.
XX
SQ Sequence 508 AA;

```
  Query Match             96.7%;  Score 2024;  DB 23;  Length 508;
  Best Local Similarity   78.1%;  Pred. No. 3.8e-204;
  Matches  397;  Conservative    1;  Mismatches    0;  Indels  110;  Gaps    1;

Qy      1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy     61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy    121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy    241 CVENEDEEGAEKKEEFQDE---------- -- - ---------- 259
          |||||||||||||||||||
Db    241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300

Qy    260 ------------------------------------------------------------ 259

Db    301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy    260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                  :|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy    311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy    371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
          |||||||||||||||||||||||||||||
Db    481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
```

RESULT 7
AAU04387
ID AAU04387 standard; Protein; 926 AA.
XX
AC AAU04387;
XX
DT 23-OCT-2001 (first entry)
XX
DE GPCR-Gs fusion protein, hRUP15-GS.
XX
KW G-protein coupled receptor; GPCR; hRUP15-Gs; agonist;
KW inverse agonist; lung cancer.
XX

OS Chimeric - Homo sapiens.
OS Chimeric - Rattus sp.
XX
PN WO200136471-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV 2000, 2000WO-US41069.
XX
PF 17-NOV-1999; 99US-0166088.
PF 17-NOV-1999; 99US-0166099.
PR 17-NOV-1999; 99US-0166369.
PF 23-DEC-1999; 99US-0171900.
PR 23-DEC-1999; 99US-0171901.
PR 23-DEC-1999; 99US-0171902.
PR 11-FEB-2000; 2000US-0181749.
PF 14-MAR-2000; 2000US-0189258.
PR 14-MAR-2000; 2000US-0189259.
PR 10-APR-2000; 2000US-0195898.
PR 10-APR-2000; 2000US-0195899.
PR 10-APR-2000; 2000US-0196078.
PR 28-APR-2000; 2000US-0200419.
PR 12-MAY-2000; 2000US-0203630.
PR 12-JUN-2000; 2000US-0210741.
PR 12-JUN-2000; 2000US-0210982.
PF 21-AUG-2000; 2000US-0226760.
PR 26-SEP-2000; 2000US-0235418.
PR 26-SEP-2000; 2000US-0235779.
PR 20-OCT-2000; 2000US-0242332.
PR 20-OCT-2000; 2000US-0242343.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Lowitz KP;
XX
DR WPI; 2001-355616/37.
DR N-PSDB; AAS08274.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents -
XX
PS Example 5; Page 151-154; 160pp; English.
XX
CC The sequence is a G-protein coupled receptor (GPCR) fusion protein,
CC hRUP15-Gs, being the human hRUP15 fused to the rat Gs protein.
CC The endogenous and non-endogenous, constitutively activated versions
CC of human G-protein coupled receptors (GPCR), are useful for direct
CC identification of candidate compounds as receptor agonists, inverse
CC agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer
CC Non-endogenous version of human GPCRs are also utilized in research
CC settings and in vitro and in vivo system, incorporating GPCRs can be
CC utilised to elucidate and understand the roles these receptors
CC play in the human condition, both normal and diseased.
XX
SQ Sequence 926 AA,

Query Match 96.7%, Score 2024; DB 22; Length 926;
Best Local Similarity 78.1%, Pred. No. 8.5e-204,
Matches 397, Conservative 1, Mismatches 0, Indels 110, Gaps 1;

```
Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQRKP 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE---------------------------------------- 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDESEFRPQHEGEVKAKEGPMEAKDGSLKAKEGSTGTSESSVEA 300

Qy     260 ---------------------------------------------------------- 259

Db     301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADYGFTEVNQCSIDLGEDDMEPGEDDI 360

Qy     260 ---------MNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                     :|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 NFSEDDVEAVNIPFSLPPSPPNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy     311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy     371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           |||||||||||||||||||||||||||||
Db     481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
```

RESULT 8
AAB61982
ID AAB61982 standard; Protein; 508 AA.
XX
AC AAB61982;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human G-protein coupled receptor, IGS1.
XX
KW G-protein coupled receptor; IGS1; psychiatric; central nervous system;
KW movement disorder; tremor; Tourette's syndrome; Parkinson's disease;
KW Huntington's disease; dyskinesia; dystonia; spasm; neuroleptic; human;
KW nootropic; anticonvulsant; relaxant; vaccine; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200109184-A1.
XX
PD 08-FEB-2001.
XX
PF 17-JUL-2000; 2000WO-EP06878.
XX
PR 15-JUL-1999; 99EP-0202326.
PR 15-JUL-1999; 99NL-1012611.
XX
PA (SOLV) SOLVAY PHARM BV.
XX
PI Deleersnijder W, Nys G, Zhang F;
XX
DR WPI; 2001-182942/18.
DR N-PSDB; AAF56818.
XX
PT Novel human G-protein coupled receptor family polypeptide, IGS1, useful
PT for treating psychiatric and central nervous system disorders such as
PT tics, tremor, Tourette's syndrome and Parkinson's disease -
XX
PS Claim 15; Page 7; 65pp; English.
XX
CC This represents a G-protein coupled receptor family polypeptide, IGS1.
CC The IGS1 protein can be expressed by standard recombinant methodology.
CC IGS1 is useful for inducing immunological response in a mammal, as
CC vaccine. IGS1 polynucleotides and polypeptides and its modulators are
CC useful for treating psychiatric and central nervous system disorders
CC especially movement disorders, such as tics, tremor, Tourette's syndrome,
CC Parkinson's disease, Huntington's disease, dyskinesias, dystonia and
CC spasms

```
XX
SQ   Sequence   508 AA;

  Query Match           96.6%;  Score 2021;  DB 22;  Length 508;
  Best Local Similarity   78.0%;  Pred. No. 7.8e-204;
  Matches  396;  Conservative    2;  Mismatches    0;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE---------------------------------------- 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300

Qy     260 ------------------------------------------------------------ 259

Db     301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDGMEFGEDDI 360

Qy     260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                   :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy     311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy     371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           |||||||||||||||||||||||||||||
Db     481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508


RESULT 9
ABB75712
ID   ABB75712 standard; Protein; 508 AA.
XX
AC   ABB75712;
XX
DT   24-JUN-2002  (first entry)
XX
DE   G-protein coupled receptor AXOR69.
XX
KW   G-protein coupled receptor; receptor; AXOR69; human; anti-HIV;
KW   virucide; antimicrobial; analgesic; cytostatic; antidiabetic;
KW   anorectic; anabolic; antiasthmatic; antiparkinsonian; cardiant;
KW   cerebroprotective; hypotensive; hypertensive; antiulcer;
KW   antiasthmatic; antiallergic; antiemetic; tranquillizer; neuroleptic;
KW   nootropic; anticonvulsant; vaccine.
XX
OS   Homo sapiens.
XX
PN   GB2367295-A.
XX
PD   03-APR-2002.
XX
PF   12-JUN-2001; 2001GB-0014287.
XX
PR   16-JUN-2000; 2000US-0596400.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Elshourbagy N,  Gattu M,  Shabon U;
XX
DR   WPI; 2002-294789/34.
DR   N-PSDB; ABL53719.
XX
PT   An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide,
PT   for treating diseases such as obesity, stroke and anxiety -
XX
PS   Claim 1; Page 27; 34pp; English.
XX
CC   The present sequence is that of human AXOR69, a G-protein coupled
CC   receptor (GPCR) that shows homology to other members of the GPCR
CC   family, such as human adrenergic alpha-1a receptor.  The invention
CC   provides AXOR69 polypeptides and polynucleotides, and methods for
CC   producing such polypeptides by recombinant techniques.  Also
CC   provided are methods for using the AXOR69 polypeptides and
CC   polynucleotides to screen for compounds that stimulate or inhibit
CC   AXOR69 levels or activity.  The polypeptides, polynucleotides,
CC   agonists and antagonists are used to treat conditions associated
CC   with AXOR69 imbalance, including bacterial, fungal, protozoan and
CC   viral infections, particularly HIV-1 and HIV-2 infections, pain,
CC   cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's
CC   disease, acute heart failure, hypotension, hypertension, urinary
CC   retention, osteoporosis, angina pectoris, myocardial infarction,
CC   stroke, ulcers, asthma, allergies, benign prostatic hypertrophy,
CC   migraine, vomiting, psychotic and neurological disorders, including
CC   anxiety, schizophrenia, manic depression, depression, delirium,
CC   dementia and severe mental retardation, and dyskinesias such as
CC   Huntington's disease and Gilles de la Tourette syndrome.  AXOR69
CC   polypeptides are also useful in vaccines, and for raising specific
CC   antibodies.
XX
SQ   Sequence   508 AA;

  Query Match           96.6%;  Score 2021;  DB 23;  Length 508;
  Best Local Similarity   78.0%;  Pred. No. 7.8e-204;
  Matches  396;  Conservative    2;  Mismatches    0;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE---------- ---------------------------- 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA 300

Qy     260 ------------------------------------------------------------ 259

Db     301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy     260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                   :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy     311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy     371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
```

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          ||||||||||||||||||||||||||||
Db    481 EDSHPDLPGIEGGTEGKIVPSYDSATFP 508


RESULT 10
AAU04384
ID   AAU04384 standard; Protein; 508 AA.
XX
AC   AAU04384;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human G-protein coupled receptor, hRUP15, mutant A398K.
XX
KW   Human, G protein coupled receptor, GPCR, hRUP15, agonist,
KW   inverse agonist; lung cancer; A398K; mutant; mutein.
XX
OS   Homo sapiens.
XX
PN   WO200136471-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US31509.
XX
PR   17-NOV-1999;   99US-0166088.
PR   17-NOV-1999;   99US-0166099.
PR   17-NOV-1999;   99US-0166369.
PR   23-DEC-1999;   99US-0171900.
PR   23-DEC-1999;   99US-0171901.
PR   23-DEC-1999;   99US-0171902.
PR   11-FEB-2000; 2000US-0181749.
PR   14-MAR-2000; 2000US-0189258.
PR   14-MAR-2000; 2000US-0189259.
PR   19-APR-2000; 2000US-0198308.
PR   10-APR-2000; 2000US-0195899.
PR   10-APR-2000; 2000US-0196078.
PR   28-APR-2000; 2000US-0200419.
PR   12-MAY-2000; 2000US-0203630.
PR   12-JUN-2000; 2000US-0210741.
PR   12-JUN-2000; 2000US-0210982.
PR   21-AUG-2000; 2000US-0226760.
PR   26-SEP-2000; 2000US-0235418.
PR   26-SEP-2000; 2000US-0235779.
PR   20-OCT-2000; 2000US-0242332.
PR   20-OCT-2000; 2000US-0242343.
XX
PA   (AREN ) ARENA PHARM INC.
XX
PI   Chen R,  Dang HT,  Lowitz KP;
XX
DR   WPI; 2001-355616/37.
DR   N-PSDB; AAS08265.
XX
PT   Endogenous and non-endogenous versions of human G-protein coupled
PT   receptors for direct identification of candidate compounds as agonists,
PT   inverse agonists or partial agonists for use as therapeutic agents -
XX
PS   Claim 38; Page 141; 160pp; English.
XX
CC   The sequence is a human G-protein coupled receptor (GPCR), hRUP15, mutant
CC   A398K. The endogenous and non-endogenous, constitutively activated
CC   versions of human G-protein coupled receptors (GPCR), are useful for
CC   direct identification of candidate compounds as receptor agonists,
CC   inverse agonists or partial agonists having applicability as therapeutic
CC   agents for treating diseases related to GPCR, e.g. lung cancer.
CC   Non-endogenous version of human GPCRs are also utilized in research
CC   settings and in vitro and in vivo system, incorporating GPCRs can be
CC   utilised to elucidate and understand the roles these receptors
CC   play in the human condition, both normal and diseased.
XX
SQ   Sequence   508 AA;
```

```
  Query Match           96.5%,  Score 2019,  DB 22;  Length 508;
  Best Local Similarity  78.0%,  Pred. No. 1.3e-203;
  Matches  396;  Conservative    1;  Mismatches    1;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVVVSVDRYLSIIHPLSYPSKMTQPPGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARPQHALLYNVKPHSLEVPVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE---------------------------------------- 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEPQDESEFPRQHEGEVKAKEGPMEAKDGSLKAKFGSTGTSESSVEA 300

Qy     260 ------------------------------------------------------------ 259

Db     301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGPTEVNQGSIDLGEDDMEFGFDDI 360

Qy     260 -------- MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                    :|||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy     311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy     371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           ||||||||||||||||||||||||||||
Db     481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508


RESULT 11
ABB07985
ID   ABB07985 standard; Protein; 508 AA.
XX
AC   ABB07985;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Human seven transmembrane receptor, 65499 protein.
XX
KW   Human; seven transmembrane domain receptor; 65499; 58875; cytostatic;
KW   osteopathic; vasotropic; cardiant; antipsoriatic; antithyroid; receptor;
KW   neuroprotective; antiparkinsonian; antidiabetic; virucide, analgesic;
KW   antirheumatic, antiarthritic, anorectic, immunomodulator; gene therapy
XX
OS   Homo sapiens.
XX
PN   WO200228901-A2.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US31250.
XX
PR   05-OCT-2000; 2000US-237700P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Gluckmann MA;
XX
DR   WPI; 2002-444096/47.
DR   N-PSDB; ABL41163, ABL41164.
XX
```

```
PT   Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane
PT   domain receptors, useful as reagents or targets for treatment or
PT   diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's
PT   disease, obesity -
XX
PS   Claim 4; Fig 1a-b; 132pp; English.
XX
CC   The invention relates to novel seven transmembrane domain receptors,
CC   designated 65499 or 58875. The 65499 and 58875 polypeptides can be
CC   expressed by standard recombinant methodology. The polypeptides, encoding
CC   polynucleotides and modulators are useful for controlling G protein
CC   coupled receptor-related disorders, and as a novel diagnostic target and
CC   therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated
CC   or related disorders such as cellular proliferative and differentiative
CC   disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism
CC   disorders (e.g., osteoporosis, rickets,), haematopoietic disorders (such
CC   as chronic myelogenous leukemia, acute promyeloid leukemia,),
CC   cardiovascular disorders (e.g., ischaemic heart disease, myocardial
CC   infarction, etc), endothelial cell disorder (e.g., psoriasis, Grave's
CC   disease,), brain disorders (e.g., multiple sclerosis, Parkinson's
CC   disease,), hormonal disorders (diabetes mellitus, hyperthyroidism,),
CC   immune disorders (including autoimmune diseases such as rheumatoid
CC   arthritis, osteoarthritis,), liver disorders, viral diseases such as
CC   hepatocellular cancer, pain disorders (e.g., pain associated with surgery
CC   or chest pain,), metabolic disorders (obesity, cachexia,). The 65499 or
CC   58875 molecules are useful as surrogate markers, as pharmacodyanamic
CC   markers and as pharmacogenomic markers. The present sequence represents
CC   the human 65499 protein.
XX
SQ   Sequence   508 AA;

  Query Match             95.7%;  Score 2002;  DB 23;  Length 508;
  Best Local Similarity   77.4%;  Pred. No. 7.8e-202;
  Matches  393;  Conservative    2;  Mismatches    3;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFPAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSPTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRPGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           |||·|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVLVSVDRYLSIIHPLSYPSKMTQRPGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAAPPQHALLYNVKRHSLEVPVKD 240
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMTWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE---------------------------------------- 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGISESSVEA 300

Qy     260 ------------------------------------------------------------ 259

Db     301 RGSEEVPESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy     260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                   :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy     311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy     371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           |||||||||||||||||||||||||||||
Db     481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508


RESULT 12
AAE15642
ID   AAE15642 standard; Protein; 485 AA.
XX
AC   AAE15642;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor-12 (GCREC-12) protein.
XX
KW   Human; G-protein coupled receptor-12; GCREC-12; therapy; cancer; stroke;
KW   cell proliferative disorder; neurological; epilepsy; Parkinson's disease;
KW   Alzheimer's disease; inflammation; thyroiditis; haemolytic anaemia; AIDS;
KW   Acquired Immune Deficiency Syndrome; dementia; nootropic; cholelithiasis;
KW   multiple sclerosis; atherosclerosis; angina pectoris; gastroenteritis;
KW   diabetes; ulcer; viral infection; immunosuppressive.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..30
FT                    /label= Signal_peptide
FT   Protein          30..485
FT                    /label= Mature_GCREC_12_protein
FT   Peptide          1..67
FT                    /label= Signal_peptide
FT   Protein          68..485
FT                    /label= Mature_GCREC_12_protein
FT   Domain           13..33
FT                    /label= Transmembrane_domain
FT   Domain           83..103
FT                    /label= Transmembrane_domain
FT   Domain           168..189
FT                    /label= Transmembrane_domain
FT   Domain           378..401
FT                    /label= Transmembrane_domain
XX
PN   WO200198351-A2.
XX
PD   27-DEC-2001.
XX
PF   15-JUN-2001; 2001WO-US19275.
XX
PR   16-JUN-2000; 2000US-212483P.
PR   22-JUN-2000; 2000US-213954P.
PR   29-JUN-2000; 2000US-215209P.
PR   07-JUL-2000; 2000US-216595P.
PR   14-JUL-2000; 2000US-218936P.
PR   19-JUL-2000; 2000US-219154P.
PR   21-JUL-2000; 2000US-220141P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Lal P,  Baughn MR,  Hafalia AJA,  Nguyen DB,  Gandhi AR,  Kallick DA;
PI   Griffin JA,  Yue H,  Khan FA,  Patterson C,  Lu DAM,  Tribouley CM;
PI   Lu Y,  Walia NK,  Graul R,  Yao MG,  Yang J,  Ramkumar J,  Au-Young J;
PI   Elliott VS,  Hernandez R,  Walsh RT,  Borowsky ML,  Thornton M,  He A;
XX
DR   WPI; 2002-075627/10.
DR   N-PSDB; AAD24967.
XX
PT   Isolated human G-protein coupled receptor polypeptides and the use of
PT   these sequences in the diagnosis, treatment and prevention of diseases
PT   and in the assessment of exogenous compounds on the expression of the
PT   receptors -
XX
PS   Claim 1; Page 125-126; 143pp; English.
XX
CC   The invention relates to isolated human G-protein coupled receptor
CC   (GCREC) polypeptides and their biologically active fragments. GCREC and
CC   protein is useful in treating a disease or condition associated with an
CC   increase or decrease in expression of functional GCREC. The GCREC's are
CC   useful in the diagnosis, treatment and prevention of cell proliferative
CC   disorders (cancer, leukaemia, melanoma); neurological disorders (stroke,
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CC   epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune
CC   inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple
CC   sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris),
CC   gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis),
CC   metabolic disorders (diabetes); viral infections (herpes virus) and in
CC   the assessment of the effects  of exogenous compounds on the expression
CC   of the nucleic acid and amino acid sequences. The present sequence is
CC   human GCREC 12 protein.
XX
SQ   Sequence   485 AA;

  Query Match             99.8%;  Score 1901;  DB 23;  Length 485;
  Best Local Similarity   77.1%;  Pred. No. 3.2e-191;
  Matches  374;  Conservative    1;  Mismatches    0;  Indels  110;  Gaps    1;

Qy         24 MPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 60

Qy         84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 120

Qy        144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 180

Qy        204 PLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDE---- 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDESEFR 240

Qy        260 ------------------------------------------------------------ 259

Db        241 RQHEGEVKAKEGRMEAKRGSLKAKEGSTGTSESSVEARGSEEVRESSTVASDGSMEGKEG 300

Qy        260 -------------------------------------------------MNIPESLPPSRRNS 273
                                                              :||||||||||||
Db        301 STKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDINFSEDDVEAVNIPESLPPSRRNS 360

Qy        274 NSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLF 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLF 420

Qy        334 FLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYD 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 FLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYD 480

Qy        394 SATFP 398
              |||||
Db        481 SATFP 485


RESULT 13
AAU25561
ID   AAU25561 standard; Protein; 204 AA.
XX
AC   AAU25561;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human G Protein-Coupled Receptor (GPCR) polypeptide #8.
XX
KW   Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
KW   attention deficit disorder; anxiety; depression; bipolar disorder;
KW   neurological disorder; Huntington's disease; dementia; obesity; anorexia;
KW   metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
KW   type 2 diabetes, cardiovascular disorder; myocardial infarction; cancer;
KW   cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
KW   viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;
KW   antidepressant; anorectic; gene therapy.
XX
OS   Homo sapiens.
XX
```

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PN   WO200162797 A2.
XX
PD   30-AUG-2001.
XX
PF   22-FEB-2001; 2001WO-US05676.
XX
PR   22-FEB-2000; 2000US-0184247.
PR   23-FEB-2000; 2000US-0184303.
PR   23-FEB-2000; 2000US-0184304.
PR   23-FEB-2000; 2000US-0184305.
PR   23 FEB 2000; 2000US-0184397.
PR   02-MAR-2000; 2000US-0186457.
PR   03 MAR-2000; 2000US-0186810.
PR   09-MAR-2000; 2000US-0188064.
PR   13-MAR-2000; 2000US-0188880.
PR   03 APR 2000; 2000US-0194344
PR   23-JUN 2000; 2000US-0213861.
PR   11-JUL-2000; 2000US-0217369.
PR   11-JUL-2000; 2000US-0217370.
PR   14 JUL 2000; 2000US-0218337.
PR   20-JUL-2000; 2000US-0218492.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Vogeli G,  Wood LS,  Parodi LA,  Lind P;
XX
DR   WPI; 2001-570628/64.
DR   N-PSDB; AAS42813.
XX
PT   New isolated nucleic acid encoding a new G-protein coupled receptor
PT   polypeptide for detecting receptor modulators that can treat mental
PT   disorders, such as schizophrenia, anxiety, depression, or obesity -
XX
PS   Claim 35; Page 73; 279pp; English
XX
CC   Sequences AAU25554-AAU25616 represent human G-protein coupled receptor
CC   (GPCR) polypeptides of the invention. The proteins and their associated
CC   DNA sequences can be used to identify compounds which bind to GPCR
CC   polypeptides and in screening for compounds that modulate GPCR activity.
CC   By screening a human subject for the presence of mutations in GPCR DNA, a
CC   GPCR-related disorder or a genetic predisposition can be diagnosed. The
CC   sequences can also be used for treatment and prevention of mental
CC   disorders such as schizophrenia, attention deficit disorder, anxiety,
CC   depression, dementia and bipolar disorder, neurological disorders such as
CC   Huntington's disease, Parkinson's disease and Tourette's syndrome,
CC   metabolic disorders such as obesity, anorexia and type 2 diabetes,
CC   cardiovascular disorders such as thrombosis, myocardial infarction,
CC   cardiomyopathy and atherosclerosis, viral infections caused by HIV and
CC   cancers.
XX
SQ   Sequence   204 AA;

  Query Match             37.9%;  Score 794;  DB 22;  Length 204;
  Best Local Similarity   99.4%;  Pred. No. 3.7e-75;
  Matches  157;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         47 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 106

Qy         61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 166

Qy        121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIV 158
              |||||||||||||||| |||||||||||||||||||||
Db        167 TIVVVSVDRYLSIIHPLFYPSKMTQRRGYLLLYGTWIV 204


RESULT 14
AAU69568
ID   AAU69568 standard; Protein; 242 AA.
XX
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AC AAU69568;
XX
DT 30-JAN-2002 (first entry)
XX
DE Human G protein-coupled receptor from cDNA Seq-2644.
XX
KW Human; G protein-coupled receptor; nGPCR; cancer; tumour;
KW thyroid disorder; myxoedema; renal failure; inflammatory condition;
KW Crohn's disease; cell differentiation disease; homeostasis disease;
KW rheumatoid arthritis; autoimmune disorder; movement disorder;
KW central nervous system disorder; stroke; Huntington's disease;
KW Tourette's syndrome; Parkinson's disease; Alzheimer's disease;
KW viral infection; HIV-1; HIV-2; human immunodeficiency virus;
KW metabolic disease; cardiovascular disease; type 2 diabetes; obesity;
KW hypotension; hypertension; thrombosis; myocardial infarction;
KW atherosclerosis; proliferative disease; hyperproliferative disorder;
KW psoriasis; hormonal disorder; polycystic ovarian syndrome;
KW alopecia; sexual dysfunction; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200177330-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US11330.
XX
PR 06-APR-2000; 2000US-195093P.
PR 06-APR-2000; 2000US-195098P.
PR 06-APR-2000; 2000US-195099P.
PR 06-APR-2000; 2000US-195148P.
PR 06-APR-2000; 2000US-195150P.
PR 06-APR-2000; 2000US-195151P.
PR 05-SEP-2000; 2000US-230149P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Vogeli G;
XX
DR WPI; 2002-010912/01.
DR N-PSDB; AAS62900.
XX
PT Novel isolated nucleic acid molecule encoding G protein-coupled
PT receptor polypeptide, nGPCR-x, useful for treating cancer, Crohn's
PT disease, rheumatoid arthritis, Alzheimer's disease, stroke, thrombosis,
PT psoriasis -
XX
PS Claim 31; Page 80; 189pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC nucleotide sequence that encodes a G protein-coupled receptor
CC polypeptide, nGPCR-x, vectors and transformed cell expressing the
CC protein, antibodies raised against the protein, modulators of the
CC protein's activity and methods of isolating the modulators. The n-GPCR is
CC for purifying a G protein from a sample containing the G protein. The
CC nucleic acid is useful for recombinantly expressing nGPCR-x receptor, for
CC detecting expression of the receptor, in the design of antisense and
CC other molecules for the suppression of the expression of nGPCR-x in a
CC cultured cell, tissue or an animal, for therapeutic purposes and to
CC provide a model for diseases of conditions characterised by aberrant
CC nGPCR-x expression, it is also useful in hybridisation assays to detect
CC the capacity of cells to express nGPCR-x, in diagnosis, to identify
CC homologues of nGPCR-x in other animals, for screening for restriction
CC fragment length polymorphism (RFLP) associated with certain disorders,
CC as well as for genetic mapping. The nucleic acid is useful in gene
CC therapy. The nGPCR is useful as a research tool for identification,
CC characterisation and purification of interacting, regulatory proteins.
CC The antibody is useful for therapeutic and diagnostic purposes, and in
CC purification of nGPCR-x. The proteins, nucleic acids and antibodies are
CC useful to treat or prevent unregulated cellular growth, such as cancer
CC cell and tumour growth, and for treating thyroid disorders (e.g.,
CC myxoedema), renal failure, inflammatory conditions (e.g., Crohn's
CC disease), diseases related to cell differentiation and homeostasis,
CC rheumatoid arthritis, autoimmune disorders, movement disorders, central
CC nervous system disorders (e.g., stroke, Huntington's disease, Tourette's
CC Syndrome, Parkinson's disease, Alzheimer's disease), infections, such as
CC viral infections caused by HIV-1 or HIV-2 (human immunodeficiency
CC virus, metabolic and cardiovascular diseases and disorders (e.g., type
CC 2 diabetes, obesity, hypotension, hypertension, thrombosis, myocardial
CC infarction, atherosclerosis), proliferative diseases and cancers,
CC hyperproliferative disorders (such as psoriasis), hormonal disorders
CC (e.g., polycystic ovarian syndrome, alopecia), and sexual dysfunction.
CC The present sequence represents an n-GPCR of the invention.
XX
SQ Sequence 242 AA;

Query Match 36.8%; Score 769.5; DB 23; Length 242;
Best Local Similarity 81.5%; Pred. No. 1.8e-72;
Matches 145; Conservative 7; Mismatches 19; Indels 7; Gaps 2;

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Qy    228 NVKRHSLEVRVKDC---VENEDEEGAEKKEEFQDE----MNIPESLPPSRRNSNSNPPLP 280
          ::|       | |   :  :| | |    | ::    :|||||||||||||||||||
Db      4 SMKADKGRTEVNQCSIDLGEDDMEFGEDDINFSEDDVEAVNIPESLPPSRRNSNSNPPLP 63

Qy    281 RCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIH 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 RCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIH 123

Qy    341 PYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 398
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 PYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 181
```

RESULT 15
AAW58586
ID AAW58586 standard; Protein; 454 AA.
XX
AC AAW58586;
XX
DT 07-SEP-1998 (first entry)
XX
DE Human histamine H2 receptor.
XX
KW Human; histamine H2 receptor; H2RH, inflammatory disease, gastric,
KW nervous condition.
XX
OS Homo sapiens.
XX
PN WO9820040-A1.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US20200.
XX
PR 07-NOV-1996; 96US-0748485.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J, Goli SK, Guegler KJ, Murry LE;
XX
DR WPI; 1998-286870/25.
DR N-PSDB; AAV37701.
XX
PT Histamine H2 receptor - used to treat inflammatory disease, gastric
PT conditions and nervous conditions
XX
PS Claim 1; Page 51-52; 77pp; English.
XX
CC The present sequence represents histamine H2 receptor (H2RH) isolated
CC from Incyte Clone 1722180 from the human bladder cDNA library
CC (BLADNOT06). A host cell, comprising a vector which contains the nucleic
CC acid encoding H2RH, can be used to produce the H2HR. An antibody which
CC specifically binds the H2RH can be used to detect and quantify H2HR in
CC a biological sample. An antagonist which specifically binds to and
CC modulates the activity of H2RH can be used in a pharmaceutical
CC composition for treating inflammatory disease, gastric conditions, and

```
CC   nervous conditions. The gastric conditions that can be treated using the
CC   antagonist, include gastritis, flu, colitis, and Crohn's disease. The
CC   nervous conditions include Alzheimer's disease, ataxia, Eaton-Lambert
CC   syndrome, epilepsy, myasthenia gravis, and Parkinson's disease. The
CC   antagonist may also be used to treat infections or inflammation of the
CC   urinary tract and bladder. It may also be used to modulate H2HR activity
CC   in endothelial cells of the cardiovascular system and treat diseases
CC   such as arteriosclerosis, cardiomyopathy, endocarditis, and ischaemia.
XX
SQ   Sequence   454 AA;

  Query Match             20.6%;  Score 430.5;  DB 19;  Length 454;
  Best Local Similarity   29.2%;  Pred. No. 2.1e-36;
  Matches   99;  Conservative   68;  Mismatches  137;  Indels   35;  Gaps    8;

Qy      31 GIIRSTVLVIFLAASFV--GNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
           |:| :  : |      ||  ||·|: : | .|  || :·|·|·|·|  .: |   || |.|
Db      25 GVIITQFIAIIVITIFVCLGNLVIVVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFV 84

Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
           | :|.   |      .|      |  | : |:. |· |  :|||  ...|: || | |  |
Db      85 VTSSIRREWIFGVVWCNFSALLYLLISSASMLTLGVIAIDRYYAVLYPMVYPMKITGNPA 144

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVIPLIVM 208
           : |   |. ...   |||.||    |||   :|   |   | ||     .   . | .||
Db     145 VMALVYIWLHSLIGCLPPLFGWSSVEFDEFKWMCVAAWHREPGYTAFWQIWCALFPFLVM 204

Qy     209 IACYSVVRCAARRQHALLYNVRRHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIPESLPP 268
           : ||  :|  ||        ||   :      || : :   :|      :   |
Db     205 LVCYGFIRRVAR--------VKAPKVHCGTVVIVEEDAQPTGVPKNS-----STSTSSSG 251

Qy     269 SRRNS------NSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY-CFLAVLAVW--VDVET 319
           ||||.      ..|       |||:   | ... .:... |||   .|  |:|    |
Db     252 SRRNAFQGVVYSAN-------QCKALITILVVLGAFMVTWGPYMVVIASEALWGKSSVSP 304

Qy     320 QVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
           : |      || |     || :||  :||::||:  |
Db     305 SLETWA----TWLSFASAVCHPLIYGLWNKTVRKELLGM 339


Search completed: February 11, 2003, 11:08:12
Job time : 86 secs
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OM protein - protein search, using sw model

Run on: February 11, 2003, 11:06:45 ; Search time 30 Seconds
(without alignments)
390.344 Million cell updates/sec

Title: US-09-841-741-2
Perfect score: 2093
Sequence: 1 MTSTCTNSTRESNSSHTCMP.....GTEGGTEGKIVPSYDSATFP 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

- Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	430.5	20.6	454	2	US-08-748-485-1	Sequence 1, Appli
2	409	19.5	529	2	US-08-467-568-2	Sequence 2, Appli
3	409	19.5	529	2	US-09-030-582-2	Sequence 2, Appli
4	409	19.5	529	5	PCT-US94-09051-2	Sequence 2, Appli
5	371.5	17.7	466	1	US-08-334-698-6	Sequence 6, Appli
6	371.5	17.7	466	1	US-08-228-932-6	Sequence 6, Appli
7	371.5	17.7	466	1	US-08-468-939-6	Sequence 6, Appli
8	371.5	17.7	466	1	US-08-722-001-28	Sequence 28, Appl
9	371.5	17.7	466	2	US-08-406-855A-6	Sequence 6, Appli
10	371.5	17.7	466	2	US-08-722-190-6	Sequence 6, Appli
11	371.5	17.7	466	3	US-08-244-354-6	Sequence 6, Appli
12	371.5	17.7	466	3	US-09-206-899-6	Sequence 6, Appli
13	371.5	17.7	466	4	US-09-444-783-6	Sequence 6, Appli
14	371.5	17.7	466	4	US-09-688-415-6	Sequence 6, Appli
15	371.5	17.7	466	5	PCT-US95-04203-6	Sequence 6, Appli
16	366.5	17.5	429	2	US-08-748-485-7	Sequence 7, Appli
17	366.5	17.5	466	1	US-08-722-001-12	Sequence 12, Appl
18	366.5	17.5	466	2	US-08-467-568-11	Sequence 11, Appl
19	366.5	17.5	466	2	US-09-030-582-11	Sequence 11, Appl
20	356.5	17.0	466	4	US-09-688-415-11	Sequence 11, Appl
21	355.5	17.0	466	2	US-08-406-855A-23	Sequence 23, Appl
22	355.5	17.0	466	3	US-09-206-899-23	Sequence 23, Appl
23	333.5	15.9	375	1	US-08-118-270-17	Sequence 17, Appl
24	333.5	15.9	375	5	PCT-US93-08528-17	Sequence 17, Appl
25	326.5	15.6	501	1	US-08-722-001-14	Sequence 14, Appl
26	326.5	15.6	501	2	US-08-467-568-9	Sequence 9, Appli
27	326.5	15.6	501	2	US-09-030-582-9	Sequence 9, Appli
28	326.5	15.6	572	1	US-08-334-698-2	Sequence 2, Appli
29	326.5	15.6	572	1	US-08-228-932-2	Sequence 2, Appli
30	326.5	15.6	572	1	US-08-468-939-2	Sequence 2, Appli
31	326.5	15.6	572	1	US-08-722-001-30	Sequence 30, Appl
32	326.5	15.6	572	2	US-08-406-855A-2	Sequence 2, Appli
33	326.5	15.6	572	2	US-08-722-190-2	Sequence 2, Appli
34	326.5	15.6	572	3	US-08-244-354-2	Sequence 2, Appli
35	326.5	15.6	572	3	US-09-206-899-2	Sequence 2, Appli
36	326.5	15.6	572	4	US-09-444-783-2	Sequence 2, Appli
37	326.5	15.6	572	4	US-09-688-415-2	Sequence 2, Appli
38	326.5	15.6	572	5	PCT-US95-04203-2	Sequence 2, Appli
39	324.5	15.5	422	1	US-07-817-920-3	Sequence 3, Appli
40	324.5	15.5	422	1	US-08-370-542-3	Sequence 3, Appli
41	324.5	15.5	422	1	US-08-117-006-3	Sequence 3, Appli
42	324.5	15.5	422	1	US-08-216-594-3	Sequence 3, Appli
43	324.5	15.5	422	1	US-08-542-358-3	Sequence 3, Appli
44	324.5	15.5	422	2	US-08-157-185-13	Sequence 13, Appl
45	324.5	15.5	422	3	US-08-281-526B-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-08-748-485-1
; Sequence 1, Application US/08748485
; Patent No. 5817480
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  NOVEL HISTAMINE H2 RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,485
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0159 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  Consensus
;      CLONE:  1722180
US-08-748-485-1

  Query Match                 20.6%;  Score 430.5;  DB 2;  Length 454;
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  Best Local Similarity   29 2%;  Pred. No  1 3e-30;
  Matches   99;  Conservative   68;  Mismatches  137;  Indels   35;  Gaps    8;

Qy       31 GIIRSTVLVIFLAASFV--GNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88

Db       25 GVIITQFIAIIVITIFVCLGNLVIVVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFV 84

Qy       89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148

Db       85 VTSSIPFEWIFGVVWCNFSALLYLLISSASMLTLGVIAIDRYYAVLYPMVYPMKITGNRA 144

Qy      149 YLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVIPLIVM 208

Db      145 VMALVYIWLHSLIGCLPPLFGWSSVEFDEFKWMCVAAWHREPGYTAFWQIWCALFPFLVM 204

Qy      209 IACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIPESLPP 268

Db      205 LVCYGFIFRVAR-------VKAPKVHCGTVVIVEEDAQRTGVPKNS----STSTSSSG 251

Qy      269 SPPNS------NSNPPLPPCYQCKAAKVIFIIIFSYVLSLGPY-CFLAVLAVW--VDVET 319

Db      252 SPRNAFQGVVYSAN----QCKALITILVVLGAFMVTWGPYMVVIASEALWGKSSVSP 304

Qy      320 QVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358

Db      305 SLETWA----TWLSFASAVCHPLIYGLWNKTVRKELLGM 339

RESULT 2
US-08-467-568-2
; Sequence 2, Application US/08467568
; Patent No. 5817477
;  GENERAL INFORMATION:
;    APPLICANT:  SOPPET, DANIEL R
;    TITLE OF INVENTION:  ADRENERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,568
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-324
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  529 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-467-568-2

  Query Match             19.5%;  Score 409;  DB 2;  Length 529;
  Best Local Similarity   28.5%;  Pred. No. 1.3e-28;
  Matches  103;  Conservative   67;  Mismatches  146;  Indels   46;  Gaps   10;

Qy        6 TNSTPE---SNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQRKP 60

Db       14 SNLTEEEGGEGASSSPSSSPSLSSP--------------FLSA--WGNLVIVVTLYKKS 56

Qy       61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Db       57 YLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVVWCNFSALLYLLISSASML 116

Qy      121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Db      117 TLGVIAIDRYYAVLYPMVYPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKW 176

Qy      181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKPHSLEVRVKD 240

Db      177 MCVAAWHREPGYTAFWQIWCALFPFLVMLVCYGFIFRVAR--------VKAPKVHCGTVV 228

Qy      241 CVENEDEEGAEKKEEFQDEMNIPESLPPSPPNSNS-NPPLPPCYQCKAAKVIFIIIFSYV 299

Db      229 IVE-EDAQRTGRK-------NSSTSTSSSGRPRNAFQGVVYSANQCKALITILVVLGAFM 280

Qy      300 LSLGPY-CFLAVLAVW--VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQ 356

Db      281 VTWGPYMVVIASEALWGKSSVSPSLETWA----TWLSFASAVCHPLIYGLWNKTVRKELL 336

Qy      357 DM 358

Db      337 GM 338

RESULT 3
US-09-030-582-2
; Sequence 2, Application US/09030582
; Patent No. 5994506
;  GENERAL INFORMATION:
;    APPLICANT:  SOPPET, DANIEL R
;    TITLE OF INVENTION:  ADRENERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,582
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/467,568
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-324
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  529 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-030-582-2

  Query Match             19.5%;  Score 409;  DB 2;  Length 529;
  Best Local Similarity   28.5%;  Pred. No. 1.3e 28;
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  Matches  103;  Conservative   67;  Mismatches  146;  Indels   46;  Gaps   10;

Qy       6 TNSTRE-----SNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
Db      14 SNLTEEEGGEGASSSPSSSPSLSSP--------------FLSA--WGNLVIVVTLYKKS 56

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
Db      57 YLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVVWCNFSALLYLLISSASML 116

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
Db     117 TLGVIAIDRYYAVLYPMVYPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKW 176

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
Db     177 MCVAAWHREPGYTAFWQIWCALFPFLVMLVCYGFIFRVAR--------VKAKKVHCGTVV 228

Qy     241 CVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNS-NPPLPRCYQCKAAKVIFIIIFSYV 299
Db     229 IVE-EDAQRTGRK------ NSSTSTSSSGRRRNAFQGVVYSANQCKALITILVVLGAFM 280

Qy     300 LSLGPY-CFLAVLAVW--VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQ 356
Db     281 VTWGPYMVVIASEALWGKSSVSPSLETWA----TWLSFASAVCHPLIYGLWNKTVRKELL 336

Qy     357 DM 358
Db     337 GM 338


RESULT 4
PCT-US94-09051-2
; Sequence 2, Application PC/TUS9409051
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Adrenergic Receptor
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS·
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09051
;      FILING DATE:  Submitted herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  529 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS·
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
PCT-US94-09051-2
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  Query Match            19.5%;  Score 409;  DB 5;  Length 529;
  Best Local Similarity  28.5%;  Pred. No. 1.3e-28;
  Matches  103;  Conservative   67;  Mismatches  146;  Indels   46;  Gaps   10;

Qy       6 TNSTRE-----SNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
Db      14 SNLTEEEGGEGASSSPSSSPSLSSP--------------FLSA--WGNLVIVVTLYKKS 56

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
Db      57 YLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVVWCNFSALLYLLISSASML 116

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
Db     117 TLGVIAIDRYYAVLYPMVYPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKW 176

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
Db     177 MCVAAWHREPGYTAFWQIWCALFPFLVMLVCYGFIFRVAR--------VKAKKVHCGTVV 228

Qy     241 CVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNS-NPPLPRCYQCKAAKVIFIIIFSYV 299
Db     229 IVE-EDAQRTGRK-------NSSTSTSSSGRRRNAFQGVVYSANQCKALITILVVLGAFM 280

Qy     300 LSLGPY-CFLAVLAVW--VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQ 356
Db     281 VTWGPYMVVIASEALWGKSSVSPSLETWA----TWLSFASAVCHPLIYGLWNKTVRKELL 336

Qy     357 DM 358
Db     337 GM 338


RESULT 5
US-08-334-698-6
; Sequence 6, Application US/08334698
; Patent No. 5556753
;  GENERAL INFORMATION:
;    APPLICANT:  Jonathan A. Bard et al.
;    TITLE OF INVENTION:  DNA Encoding Human Alpha 1 Adrenergic
;    TITLE OF INVENTION:  Receptors and Uses Thereof
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOPER & DUNHAM
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/334,698
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/952,798
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  37690I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  (212) 422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-334-698-6

Query Match 17.7%; Score 371.5; DB 1; Length 466;
Best Local Similarity 26.9%; Pred. No. 2.5e-25;
Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

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Qy      8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
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Db      5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy     68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
           :| || | |||  | | |:    |  :|     ||    .:  |   ||.  : ..|:
Db     63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy    128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
          |||: : :|| ||: :|||||  : |   | :::: |  ||:|| | |   |    :| :
Db    123 DRYIGVSYPLRYPTIVTQPRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy    188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARPQ----HALLYNVKPHSLEVPVKDCVE 243
            | | : |    :|| : ·  |  |:  |.|·     · |   |  | ·| ··   :
Db    180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHPK 239

Qy    244 NEDEEG·····AEKKEEFQDEMNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
          |    |      |: |  |   :     |  ||                 ||||  : |::  :
Db    240 NAPAGGSGMASAKTKTHFSVPL ····LKFSREK·········· ·· ·KAAKTLGIVVGCF 281

Qy    299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
          ||   |· || ·      · :  : |  |· || :|  ||:|  :|    ·  ||  |·:
Db    282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy    359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
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Db    341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385
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RESULT 6
US-08-228-932-6
; Sequence 6, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,932
; FILING DATE: 13-APR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-932-6

Query Match 17.7%; Score 371.5; DB 1; Length 466;
Best Local Similarity 26.9%; Pred. No. 2.5e-25;
Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

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Qy      8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
          |   |·||·   |    |···· |·  ·|   ·    :|||·· | :     |  ||:
Db      5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy     68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
           :| || | |||  | | |:    |  ·|     ||    ··  |   ||  ·   |
Db     63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy    128 DRYLSIIHPLSYPSKMTQRPGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
          |||. . .|| ||: :|||||  ·  |   |    ·  ·|  || || | |  |   :| :
Db    123 DRYIGVSYPLRYPTIVTQPRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy    188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARPQ--- HALLYNVKPHSLEVPVKDCVE 243
            | | : | :    :|| :..  | |.  |:|:     . |   |  | .|  ..  .
Db    180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHPK 239

Qy    244 NEDEEG-----AEKKEEFQDEMNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
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Db    240 NAPAGGSGMASAKTKTHFSVPL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy    299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
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Db    282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy    359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
          |· ·  |···  |       ||     ||  ·  · :|      ||
Db    341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385
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RESULT 7
US-08-468-939-6
; Sequence 6, Application US/08468939
; Patent No. 5714381
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,939
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 6:

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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-468-939-6

  Query Match             17.7%;  Score 371.5;  DB 1;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 2.5e-25;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 8
US-08-722-001-28
; Sequence 28, Application US/08722001
; Patent No. 5760054
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Wayne J.
;    APPLICANT:  Huff, Joel R.
;    APPLICANT:  Nerenberg, Jennie B.
;    APPLICANT:  Lee, Hee-Yoon
;    APPLICANT:  Bell, Ian M.
;    TITLE OF INVENTION:  ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  126 Lincoln Avenue
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/722,001
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/229,276
;      FILING DATE:  14-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19169Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-3462
;      TELEFAX:  (908)594-4720
;      TELEX:  138825
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-722-001-28

  Query Match             17.7%;  Score 371.5;  DB 1;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 2.5e-25;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 9
US-08-406-855A-6
; Sequence 6, Application US/08406855A
; Patent No. 5861309
;  GENERAL INFORMATION:
;    APPLICANT:  Jonathan A. Bard et al.
;    TITLE OF INVENTION:  DNA Encoding Human Alpha 1 Adrenergic
;    TITLE OF INVENTION:  Receptors and Uses Thereof
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/406,855A
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      FILING DATE:  21-AUG-1995
      CLASSIFICATION:  435
    ATTORNEY/AGENT INFORMATION
      NAME.  White, John P.
      REGISTRATION NUMBER.  28,678
      REFERENCE/DOCKET NUMBER.  41337 A PCT US/JPW/KDB
    TELECOMMUNICATION INFORMATION.
      TELEPHONE:  (212) 278-0400
      TELEFAX.  (212) 391 0526
;  INFORMATION FOR SEQ ID NO.  6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  466 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-406-855A-6

  Query Match              17.7%,  Score 371.5,  DB 2,  Length 466;
  Best Local Similarity    26.9%;  Pred  No  2.5e-25;
  Matches  109;  Conservative   77,  Mismatches  180,  Indels   39,  Gaps   11;

Qy      8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db      5 SGNASDSSNCTQP  PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy     68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db     63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy    128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db    123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI- N 179

Qy    188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db    180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy    244 NEDEEG----AEKKEEFQDEMNIPESLPPSFRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db    240 NAPAGGSGMASAKTKTHFSVRL----LKFSREK----------  KAAKTLGIVVGCF 281

Qy    299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db    282 VLCWLPF FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy    359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
Db    341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385

RESULT 10
US-08-722-190-6
; Sequence 6, Application US/08722190
; Patent No. 5990128
;  GENERAL INFORMATION.
;    APPLICANT:  Charles Gluchowski, Carlos C. Forray, George
;    APPLICANT.  Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
;    TITLE OF INVENTION.  USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
;    TITLE OF INVENTION.  TREAT BENIGN PROSTATIC HYPERPLASIA
;    NUMBER OF SEQUENCES.  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOPER & DUNHAM LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA.
;      APPLICATION NUMBER:  US/08/722,190
;      FILING DATE:  4-APR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41878-D-PCT/JPW/AGL
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX.  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH.  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-722-190-6

  Query Match              17.7%,  Score 371.5,  DB 2;  Length 466;
  Best Local Similarity    26.9%;  Pred. No. 2.5e-25;
  Matches  109,  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy      8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db      5 SGNASDSSNCTQP  PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy     68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db     63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy    128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db    123 DPYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy    188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db    180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy    244 NEDEEG----AEKKEEFQDEMNIPESLPPSFRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db    240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK-----------  KAAKTLGIVVGCF 281

Qy    299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db    282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy    359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
Db    341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385

RESULT 11
US-08-244-354-6
; Sequence 6, Application US/08244354
; Patent No. 6015819
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Gluchowski, et al.
;    TITLE OF INVENTION.  USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
;    TITLE OF INVENTION:  TREAT BENIGN PROSTATIC HYPERPLASIA
;    NUMBER OF SEQUENCES.  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOPER & DUNHAM LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE.  PatentIn Release #1.24
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,354
;      FILING DATE:  April 1, 1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41878-D-PCT-US/JPW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-244-354-6

  Query Match             17.7%;  Score 371.5;  DB 3;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 2.5e-25;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHPK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRPNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK-------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 12
US-09-206-899-6
; Sequence 6, Application US/09206899
; Patent No. 6083705
;  GENERAL INFORMATION:
;    APPLICANT:  Jonathan A. Bard et al.
;    TITLE OF INVENTION:  DNA Encoding Human Alpha 1 Adrenergic
;    TITLE OF INVENTION:  Receptors and Uses Thereof
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/206,899
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/406,855
;      FILING DATE:  21-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41337-A-PCT-US/JPW/KDB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0526
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-206-899-6

  Query Match             17.7%;  Score 371.5;  DB 3;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 2.5e-25;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCPVYVVAKPESRGLKSGLKTDKSDSEQVTLPIHPK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK-------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 13
US-09-444-783-6
; Sequence 6, Application US/09444783
; Patent No. 6420389
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Gluchowski, et al.
;    TITLE OF INVENTION:  USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
;    TITLE OF INVENTION:  TREAT BENIGN PROSTATIC HYPERPLASIA
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOPER & DUNHAM LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U S A
;      ZIP:  10036
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.24
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/444,783
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  White, John P.
;       REGISTRATION NUMBER:  28,678
;       REFERENCE/DOCKET NUMBER:  41878 AA PCT US/JPW
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 278-0400
;       TELEFAX:  (212) 391-0525
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  466 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-444-783-6

  Query Match             17.7%;  Score 371.5;  DB 4;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 2.5e-25;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy          8 STPESNSSHTCMPLSKMPISLAHGIIFSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
                |   |:||.   |     |.      |.   :|         ||||.:  |      |  ||
Db          5 SGNASDSSNCTQP-PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy         68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
                :| || |  |||  | |  |        |  :|       ||       ::  |    ||: : ::|:
Db         63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy        128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
              |||:    :|  ||  :|||||   |     |        :   ||:||  |  |   |   :|  :
Db        123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy        188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
                 | | : | :      :||  :   |  |:   |       |    |     |
Db        180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy        244 NEDEEG----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
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Qy        299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
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Db        282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy        359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
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Db        341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVPIPVGSRETF 385

RESULT 14
US-09-688-415-6
; Sequence 6, Application US/09688415
; Patent No. 6448011
; GENERAL INFORMATION:
;  APPLICANT:  Bard, Jonathan A
;  APPLICANT:  Forray, Carlos
;  APPLICANT:  Weinshank, Richard L
;  TITLE OF INVENTION:  DNA ENCODING HUMAN ALPHA 1 ADRENERGIC RECEPTORS AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  41337aza
;  CURRENT APPLICATION NUMBER:  US/09/688,415
;  CURRENT FILING DATE:  2000-10-16
;  PRIOR APPLICATION NUMBER:  09/474,551
;  PRIOR FILING DATE:  1999-12-29
;  NUMBER OF SEQ ID NOS:  23
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-688-415-6

  Query Match             17.7%;  Score 371.5;  DB 4;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 2.5e-25;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy          8 STPESNSSHTCMPLSKMPISLAHGIIFSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
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Db          5 SGNASDSSNCTQP-PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy         68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
                :| || |  |||  | |  |        |  :|       ||       ::  |    ||: : ::|:
Db         63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy        128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
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Qy        188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
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Db        180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy        244 NEDEEG----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
                |     |      |:  |    |       |  ||               ||||  :  |:  ·
Db        240 NAPAGGSGMASAKTKTHFSVRL-----LKFSPEK-------------KAAKTLGIVVGCF 281

Qy        299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
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Db        282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy        359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
              |.   |       |       ||      ||       :  :|      ||
Db        341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKDMVPIPVGSRETF 385

RESULT 15
PCT-US95-04203-6
; Sequence 6, Application PC/TUS9504203
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Gluchowski, Carlos C. Forray, George
;    APPLICANT:  Chiu, Theresa A  Branchek, John M. Wetzel and Paul R. Hartig
;    TITLE OF INVENTION:  USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
;    TITLE OF INVENTION:  TREAT BENIGN PROSTATIC HYPERPLASIA
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOPER & DUNHAM LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04203
;      FILING DATE:  4-APR-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41878-D-PCT/JPW/AGL
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04203-6

Query Match 17.7%; Score 371.5; DB 5; Length 466;
Best Local Similarity 26.9%; Pred. No. 2.5e-25;
Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

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Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKPHSLEVPVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK-------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
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Job time : 33 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 11, 2003, 11:08:20 ; Search time 13 Seconds
(without alignments)
782.189 Million cell updates/sec

Title: US-09-841-741-2
Perfect score: 2093
Sequence: 1 MTSTCTNSTRESNSSHTCMP.....GTEGGTEGKIVPSYDSATFP 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2024	96.7	508	9	US-09-791-932-112	Sequence 112, App
2	794	37.9	204	9	US-09-791-932-68	Sequence 68, Appl
3	769.5	36.8	242	10	US-09-828-644-115	Sequence 115, App
4	409	19.5	529	10	US-09-951-622-2	Sequence 2, Appli
5	371.5	17.7	466	9	US-10-185-991-6	Sequence 6, Appli
6	366.5	17.5	466	10	US-09-951-622-11	Sequence 11, Appl
7	326.5	15.6	501	10	US-09-951-622-9	Sequence 9, Appli
8	326.5	15.6	572	9	US-10-185-991-2	Sequence 2, Appli
9	324.5	15.5	422	9	US-10-166-101-3	Sequence 3, Appli
10	321	15.3	451	10	US-09-993-844-6	Sequence 6, Appli
11	319	15.2	497	12	US-10-052-589-2	Sequence 2, Appli
12	319	15.2	517	10	US-09-951-622-10	Sequence 10, Appl
13	319	15.2	520	9	US-10-185-991-4	Sequence 4, Appli
14	299	14.3	259	9	US-10-080-960-25	Sequence 25, Appl
15	299	14.3	259	9	US-10-012-140-27	Sequence 27, Appl
16	299	14.3	259	9	US-10-012-140-29	Sequence 29, Appl
17	299	14.3	259	9	US-10-077-698-3	Sequence 3, Appli
18	299	14.3	259	10	US-09-796-338A-23	Sequence 23, Appl
19	297	14.2	445	10	US-09-989-861-16	Sequence 16, Appl
20	287	13.7	241	10	US-09-864-761-38226	Sequence 38226, A
21	277	13.2	460	10	US-09-989-861-18	Sequence 18, Appl
22	275	13.1	460	9	US-10-166-101-4	Sequence 4, Appli
23	274.5	13.1	400	10	US-09-895-211-4	Sequence 4, Appli
24	274.5	13.1	400	10	US-09-895-211-6	Sequence 6, Appli
25	270	12.9	388	10	US-09-989-861-8	Sequence 8, Appli
26	268.5	12.8	470	9	US-10-166-101-8	Sequence 8, Appli
27	268.5	12.8	471	8	US-08-681-219-30	Sequence 30, Appl
28	268.5	12.8	471	10	US-09-929-313-2	Sequence 2, Appli
29	267.5	12.8	413	10	US-09-811-286-2	Sequence 2, Appli
30	267.5	12.8	413	10	US-09-951-622-12	Sequence 12, Appl
31	267.5	12.8	413	10	US-09-993-844-2	Sequence 2, Appli
32	267.5	12.8	413	10	US-09-990-596-1	Sequence 1, Appli
33	267.5	12.8	413	10	US-09-922-494-13	Sequence 13, Appl
34	267.5	12.8	431	9	US-10-029-009-8	Sequence 8, Appli
35	267.5	12.8	451	9	US-10-029-009-20	Sequence 20, Appl
36	261.5	12.5	471	10	US-09-929-313-4	Sequence 4, Appli
37	261	12.5	387	10	US-09-989-861-2	Sequence 2, Appli
38	261	12.5	406	10	US-09-989-861-4	Sequence 4, Appli
39	261	12.5	601	10	US-09-782-980-84	Sequence 84, Appl
40	261	12.5	601	10	US-09-884-430-8	Sequence 8, Appli
41	259	12.4	222	10	US-09-911-005-4	Sequence 4, Appli
42	259	12.4	366	9	US-09-992-331-9	Sequence 9, Appli
43	259	12.4	382	10	US-09-993-844-5	Sequence 5, Appli
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45	258	12.3	366	9	US-09-992-331-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-791-932-112
; Sequence 112, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1el G Protein-Coupled Receptors Cross-Referenc
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861

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;  PRIOR FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER:  60/194,344
;  PRIOR FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:  60/218,337
;  PRIOR FILING DATE:  2000-07-14
;  NUMBER OF SEQ ID NOS:  184
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 112
;  LENGTH: 508
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-791-932-112

  Query Match             96.7%;  Score 2024;  DB 9;  Length 508;
  Best Local Similarity   78.1%;  Pred. No. 1.2e-176;
  Matches  397;  Conservative    1;  Mismatches    0;  Indels  110;  Gaps    1;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240

Qy     241 CVENEDEEGAEKKEEFQDE---------- ---------- 259
           |||||||||||||||||||
Db     241 CVENEDEEGAEKKEEFQDESEFPPQHEGEVKAKEGPMEAKDGSLKAKEGSTGTSESSVEA 300

Qy     260 ------------------------------------------------------------ 259

Db     301 PGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360

Qy     260 ---------MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
                   :||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 NFSEDDVEAVNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 420

Qy     311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480

Qy     371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           |||||||||||||||||||||||||||||
Db     481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508


RESULT 2
US-09-791-932-68
; Sequence 68, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
;  APPLICANT:  Vogeli, Gabriel
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Hiebsch, Ronald R.
;  APPLICANT:  Lind, Peter
;  APPLICANT:  Kaytes, Paul S.
;  APPLICANT:  Ruff, Valerie
;  APPLICANT:  Huff, Rita M.
;  APPLICANT:  Wood, Linda S.
;  TITLE OF INVENTION:  No. US20030003451A1el G Protein-Coupled Receptors Cross-Referen
;  FILE REFERENCE:  00325 US1
;  CURRENT APPLICATION NUMBER: US/09/791,932
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER:  60/184,305
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,304
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,303
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,397
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/184,247
;  PRIOR FILING DATE:  2000-02-23
;  PRIOR APPLICATION NUMBER:  60/188,880
;  PRIOR FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER:  60/217,369
;  PRIOR FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER:  60/217,370
;  PRIOR FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER:  60/218,492
;  PRIOR FILING DATE:  2000-07-20
;  PRIOR APPLICATION NUMBER:  60/186,810
;  PRIOR FILING DATE:  2000-03-03
;  PRIOR APPLICATION NUMBER:  60/188,064
;  PRIOR FILING DATE:  2000-03-09
;  PRIOR APPLICATION NUMBER:  60/186,457
;  PRIOR FILING DATE:  2000-03-02
;  PRIOR APPLICATION NUMBER:  60/213,861
;  PRIOR FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER:  60/194,344
;  PRIOR FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:  60/218,337
;  PRIOR FILING DATE:  2000-07-14
;  NUMBER OF SEQ ID NOS:  184
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 68
;  LENGTH: 204
;  TYPE: PRT
;  ORGANISM. Homo sapiens
US-09-791-932-68

  Query Match             37.9%;  Score 794;  DB 9;  Length 204;
  Best Local Similarity   99.4%;  Pred. No. 4.4e-65;
  Matches  157;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 106

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 166

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIV 158
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Db     167 TIVVVSVDRYLSIIHPLFYPSKMTQRRGYLLLYGTWIV 204


RESULT 3
US-09-828-644-115
; Sequence 115, Application US/09828644
; Patent No. US20020015998A1
; GENERAL INFORMATION:
;  APPLICANT: Vogeli, Gabriel
;  TITLE OF INVENTION: No. US20020015998A1el G Protein-Coupled Receptors
;  FILE REFERENCE: 00196US1
;  CURRENT APPLICATION NUMBER: US/09/828,644
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: 60/195,150
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,099
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,151
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,148
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,093
;  PRIOR FILING DATE: 2000-04-06
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;  PRIOR APPLICATION NUMBER: 60/195,098
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/230,149
;  PRIOR FILING DATE: 2000-09-05
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-828-644-115

  Query Match             36.8%;  Score 769.5;  DB 10;  Length 242;
  Best Local Similarity   81.5%;  Pred. No. 9.4e-63;
  Matches  145;  Conservative    7;  Mismatches   19;  Indels    7;  Gaps    2;

Qy     228 NVKRHSLEVRVKDC---VENEDEEGAEKKEEFQDE----MNIPESLPPSRRNSNSNPPLP 280
           ::|        |  |    :  :| |  |    | ::    :|||||||||||||||||||
Db       4 SMKADKGRTEVNQCSIDLGEDDMEFGEDDINFSEDDVEAVNIPESLPPSRRNSNSNPPLP 63

Qy     281 RCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIH 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 RCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIH 123

Qy     341 PYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 398
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 PYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 181


RESULT 4
US-09-951-622-2
; Sequence 2, Application US/09951622
; Patent No. US20020106734A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel R. Soppet et al.
;  TITLE OF INVENTION: ADRENERGIC RECEPTOR
;  FILE REFERENCE: PF128D2C1
;  CURRENT APPLICATION NUMBER: US/09/951,622
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/339,244
;  PRIOR FILING DATE: 1999-06-24
;  PRIOR APPLICATION NUMBER: 09/030,582
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 08/467,568
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US94/09051
;  PRIOR FILING DATE: 1994-08-10
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 529
;   TYPE: PRT
;   ORGANISM: human
US-09-951-622-2

  Query Match             19.5%;  Score 409;  DB 10;  Length 529;
  Best Local Similarity   28.5%;  Pred. No. 1.8e-29;
  Matches  103;  Conservative   67;  Mismatches  146;  Indels   46;  Gaps   10;

Qy       6 TNSTRE-----SNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
             :| | |     ::|| :  |    |                ||:|   ||:|: : | :|
Db      14 SNLTEEEGGEGASSSPSSSPSLSSP--------------FLSA--WGNLVIVVTLYKKS 56

Qy      61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
             || ::|:|:|:| ::: |   || |:|| :|:   |     :|     |  | : ||:
Db      57 YLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVVWCNFSALLYLLISSASML 116

Qy     121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
           |: |:::||| ::::|: || |:|  |  : |   |: :::   |||:||   : |
Db     117 TLGVIAIDRYYAVLYPMVYPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKW 176

Qy     181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
           :|   |   | ||    :   : | :||: ||  :|  ||         ||   :

Db     177 MCVAAWHREPGYTAFWQIWCALFPFLVMLVCYGFIFRVAR--------VKAPKVHCGTVV 228

Qy     241 CVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNS-NPPLPRCYQCKAAKVIFIIIFSYV 299
             || || :   :|        |   |   | |  |:     :    ||||   | ::: :::
Db     229 IVE-EDAQRTGRK-------NSSTSTSSSGRRRNAFQGVVYSANQCKALITILVVLGAFM 280

Qy     300 LSLGPY-CFLAVLAVW--VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQ 356
           :: |||   :|  |:|     |   :  |      || |     || :||  :||::||:
Db     281 VTWGPYMVVIASEALWGKSSVSPSLETWA----TWLSFASAVCHPLIYGLWNKTVRKELL 336

Qy     357 DM 358
           |
Db     337 GM 338


RESULT 5
US-10-185-991-6
; Sequence 6, Application US/10185991
; Publication No. US20030022900A1
;   GENERAL INFORMATION:
;        APPLICANT: Charles Gluchowski, et al.
;        TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
;                            TREAT BENIGN PROSTATIC HYPERPLASIA
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: COOPER & DUNHAM LLP
;             STREET: 1185 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: U.S.A.
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.24
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/185,991
;             FILING DATE: 28-Jun-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/444,783
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: White, John P.
;             REGISTRATION NUMBER: 28,678
;             REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 278-0400
;             TELEFAX: (212) 391-0525
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 466 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-185-991-6

  Query Match             17.7%;  Score 371.5;  DB 9;  Length 466;
  Best Local Similarity   26.9%;  Pred. No. 4.1e-26;
  Matches  109;  Conservative   77;  Mismatches  180;  Indels   39;  Gaps   11;

Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
           |   |:||:   |    |:::: |:  :|  :    :|||:: | :     |  ||:
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
             :| || | |||  | | |:     |  :|     ||    ::  |   ||:  : ::|:
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
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Db    123 DPYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy    188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243

Db    180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy    244 NEDEEG---AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298

Db    240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy    299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358

Db    282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy    359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397

Db    341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 6
US-09-951-622-11
; Sequence 11, Application US/09951622
; Patent No. US20020106734A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel R. Soppet et al.
;  TITLE OF INVENTION: ADRENERGIC RECEPTOR
;  FILE REFERENCE: PF128D2C1
;  CURRENT APPLICATION NUMBER: US/09/951,622
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/339,244
;  PRIOR FILING DATE: 1999-06-24
;  PRIOR APPLICATION NUMBER: 09/030,582
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 08/467,568
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US94/09051
;  PRIOR FILING DATE: 1994-08-10
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: human
US-09-951-622-11

  Query Match           17.5%;  Score 366.5;  DB 10;  Length 466;
  Best Local Similarity   26.7%;  Pred. No. 1.2e-25;
  Matches  109;  Conservative   76;  Mismatches  182;  Indels   39;  Gaps   10;

Qy      8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67

Db      5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy     68 PFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127

Db     63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy    128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187

Db    123 DPYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy    188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243

Db    180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy    244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298

Db    240 NAPAGGSGMASAKTKTHFSVPL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy    299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358

Db    282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy    359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397

Db    341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 7
US-09-951-622-9
; Sequence 9, Application US/09951622
; Patent No. US20020106734A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel R. Soppet et al.
;  TITLE OF INVENTION: ADRENERGIC RECEPTOR
;  FILE REFERENCE: PF128D2C1
;  CURRENT APPLICATION NUMBER: US/09/951,622
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: 09/339,244
;  PRIOR FILING DATE: 1999-06-24
;  PRIOR APPLICATION NUMBER: 09/030,582
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 08/467,568
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US94/09051
;  PRIOR FILING DATE: 1994-08-10
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: human
US-09-951-622-9

  Query Match           15.6%;  Score 326.5;  DB 10;  Length 501;
  Best Local Similarity   27.7%;  Pred. No. 5.6e-22;
  Matches   96;  Conservative   58;  Mismatches  157;  Indels   35;  Gaps   10;

Qy     29 AHGIIPSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88

Db     52 AQGVGVGVFLAAFILMAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLPFS 111

Qy     89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148

Db    112 ATMEVLGFWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 171

Qy    149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207

Db    172 AAILALLWVVALVVSVGPLLGWKEPVFPDER--FCGITEEA--GYAVFSSVCSFYLPMAV 227

Qy    208 MIACYSVVFCAAR-RQHALLYNVKRHS-----LEVRVKDCVENEDEEGAE----KKE 254

Db    228 IVVMYCRVYVVARSTTPSLRAGVKRERGKASEVVLRIHCRGAATGAD--GAHGMPSAKGH 285

Qy    255 EFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVW 314

Db    286 TFRSSLSV-RLLKFSREK------------KAAKTLAIVVGVFVLCWFPFFFVLPLGS- 330

Qy    315 VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360

Db    331 LFPQLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLP 376


RESULT 8
US-10-185-991-2
; Sequence 2, Application US/10185991
; Publication No. US20030022900A1
;   GENERAL INFORMATION:
;        APPLICANT: Charles Gluchowski, et al.
;        TITLE OF INVENTION. USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
;                           TREAT BENIGN PROSTATIC HYPERPLASIA
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: COOPER & DUNHAM LLP
;             STREET: 1185 Avenue of the Americas
```

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;              CITY: New York
;              STATE: New York
;              COUNTRY: U.S.A.
;              ZIP: 10036
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.24
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/185,991
;              FILING DATE: 28-Jun-2002
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/444,783
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: White, John P.
;              REGISTRATION NUMBER: 28,678
;              REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212) 278-0400
;              TELEFAX: (212) 391-0525
;              TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 2.
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 572 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-185-991-2

  Query Match             15.6%;  Score 326.5;  DB 9;  Length 572;
  Best Local Similarity   27.7%;  Pred. No. 6.7e-22;
  Matches   96;  Conservative   58;  Mismatches  157;  Indels   35;  Gaps   10;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
           | |:      |   |:   :  ||::: | :     |  ||| || || | |||  : | |:
Db      94 AQGVGVGVFLAAFILMAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLPFS 153

Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
             |  ||      ||     ::  |    ||: ::  :|||||: : | | ||: ||:|:
Db     154 ATMEVLGFWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 213

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207
           :|    |:||::  |  || || :    |||   | :   |   | : | |     :|: |
Db     214 AAILALLWVVALVVSVGPLLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLPMAV 269

Qy     208 MIACYSVVFCAAR-RQHALLYNVKRHS-------LEVRVKDCVENEDEEGAE-----KKE 254
           ::  |  |:  ||    :|   |||          | :  :       |  ||       |
Db     270 IVVMYCRVYVVARSTTRSLEAGVKRERGKASEVVLRIHCRGAATGAD--GAHGMRSAKGH 327

Qy     255 EFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVW 314
            |:  :::   |  ||                |||| : |::  :||   |: |:  |
Db     328 TFRSSLSV-RLLKFSREK-------------KAAKTLAIVVGVFVLCWFPFFFVLPLGS- 372

Qy     315 VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
           :  : :  : |  :| || :   |::| :|    :  |:    :|:
Db     373 LFPQLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 418


RESULT 9
US-10-166-101-3
; Sequence 3, Application US/10166101
; Publication No. US20030008823A1
; GENERAL INFORMATION:
;  APPLICANT: Weinshank, Richard L.
;  APPLICANT:  Branchek, Theresa
;  APPLICANT:  Hartig, Paul
;  TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
;  FILE REFERENCE: 39318-c
;  CURRENT APPLICATION NUMBER: US/10/166,101
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: 09/246,075
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 08/483,222
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/117,006
;  PRIOR FILING DATE: 1994-08-22
;  PRIOR APPLICATION NUMBER: PCT/US93/00149
;  PRIOR FILING DATE: 1993-01-08
;  PRIOR APPLICATION NUMBER: 07/817,920
;  PRIOR FILING DATE: 1992-01-08
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-166-101-3

  Query Match             15.5%;  Score 324.5;  DB 9;  Length 422;
  Best Local Similarity   24.0%;  Pred. No. 6.9e-22;
  Matches   95;  Conservative   72;  Mismatches  170;  Indels   59;  Gaps    7;

Qy      26 ISLAHGIIRSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 83
           ::::: :| | :|   :  : :||  :| |: |:|   |  | |  | :| ||||:   |
Db      31 VTVSYQVITSLLLGTLIFCAVLGNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88

Qy      84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
           | |       |   | |     |   ::|  |   :|:  :  :::||| :|  |: | :|
Db      89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148

Qy     144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
           | ||   |:  ||::  | | ||: ||    ::|:   :        ||| |       |
Db     149 TPRRAAALISLTWLIGFLISIPPMLGWRTP--EDRSDPDACTISKDHGYTIYSTFGAFYI 206

Qy     204 PLIVMIACYSVVFCAAR-RQHALLYNVKRHSLEVR------------------------- 237
           ||::|:  |  :| ||| |    :  |::   : |
Db     207 PLLLMLVLYGRIFRAARFRIRKTVKKVEKTGADTRHGASPAPQPKKSVNGESGSRNWRLG 266

Qy     238 ----------VKDCVENEDEEGAEKKEEFQDEMNIPESLP-PS----------------R 270
                       |   |:  |  :  |      |  | || ||
Db     267 VESKAGGALCANGAVRQGDDGAALEVIEVHRVGNSKEHLPLPSEAGPTPCAPASFERKNE 326

Qy     271 RNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIII 330
           ||: :   :    : |  | : ||: :::|   |:  :|::  : :    :|  :  ||
Db     327 RNAEAKRKMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCESSCHMPTLLGAIIN 386

Qy     331 WLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKE 366
           || :    ::| :| | :|  :    : ::|  ||::
Db     387 WLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCLFCRQ 422


RESULT 10
US-09-993-844-6
; Sequence 6, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
;  APPLICANT: Oakley, Robert H.
;  APPLICANT:  Barak, Lawrence S.
;  APPLICANT:  Laporte, Stephane A.
;  APPLICANT:  Caron, Marc G.
;  TITLE OF INVENTION: Modified G-Protein Coupled Receptors
;  FILE REFERENCE: 033072-026
;  CURRENT APPLICATION NUMBER: US/09/993,844
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: US 60/245,772
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: US 60/260,363
;  PRIOR FILING DATE: 2001-01-08
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 451
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: amino acid sequence of 5HT1AR-V2R chimera
;   OTHER INFORMATION: expressed from the pEArrB-1/5HT1AR vector
US-09-993-844-6

  Query Match             15.3%;  Score 321;  DB 10;  Length 451;
  Best Local Similarity   23.5%;  Pred. No. 1.6e-21;
  Matches  100;  Conservative   72;  Mismatches  182;  Indels   72;  Gaps    8;

Qy         26 ISLAHGIIPSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNPFIFNLLVTDLLQISL 83
Db         31 VTVSYQVITSLLLGTLIFCAVLGNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88

Qy         84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
Db         89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148

Qy        144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
Db        149 TPRRAAALISLTWLIGFLISIPPMLGWPTP--EDPSDPDACTISKDHGYTIYSTFGAFYI 206

Qy        204 PLIVMIACYSVVFCAAR-RQHALLYNVFRHSLEVR --------------------- 237
Db        207 PLLLMLVLYGRIFRAARFRIPKTVKKVEKTGADTPHGASPAPQPKKSVNGESGSRNWRLG 266

Qy        238             VKDCVENEDEEGAEKKEEFQDEMNIPESLP-PS ---------------P 270
Db        267 VESKAGGALCANGAVRQGDDGAALEVIEVHRVGNSKEHLPLPSEAGPTPCAPASFERKNE 326

Qy        271 RNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIII 330
Db        327 RNAEAKRKMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCESSCHMPTLLGAIIN 386

Qy        331 WLFPLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVP 390
Db        387 WLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCNFC------------AAAPGRTPPSLGP 433

Qy        391 SYDSAT 396
Db        434 QDESCT 439

RESULT 11
US-10-052-589-2
; Sequence 2, Application US/10052589
; Patent No. US20020133832A1
; GENERAL INFORMATION:
;  APPLICANT: Perez, Dianne
;  APPLICANT: Zuscik, Michael
;  TITLE OF INVENTION: Model systems for neurodegenerative and cardiovascular disorders
;  FILE REFERENCE: 26473/04200
;  CURRENT APPLICATION NUMBER: US/10/052,589
;  CURRENT FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: US 09/568,255
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Mesocricetus sp.
US-10-052-589-2

  Query Match             15.2%;  Score 319;  DB 12;  Length 497;
  Best Local Similarity   26.0%;  Pred. No. 2.7e-21;
  Matches   92;  Conservative   70;  Mismatches  162;  Indels   30;  Gaps    7;

Qy         14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
Db         32 SSNSTLPQLDVTRAISVGL----VLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87

Qy         74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
Db         88 AIADLLLSFTVLPFSATLEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147

Qy        134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
Db        148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204

Qy        194 ILSVVSFIVIPLIVMIACYSVVFCAAPPQHALL------YNVKPHSLEVPVKDCVENE 245
Db        205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262

Qy        246 DEEGAEKKEEFQDEMNIPESLPPSPRPNSNSNPPLPPCYQCKAAKVIFIIIFSYVLSLGPY 305
Db        263 DTLSSTKAKGHNPRSSIAVKLFKFSREK-----------KAAKTLGIVVGMFILCWLPF 310

Qy        306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDML 359
Db        311 -FIALPLGSLFSTLKPPDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKRAFMRIL 363

RESULT 12
US-09-951-622-10
; Sequence 10, Application US/09951622
; Patent No. US20020106734A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel R. Soppet et al.
;  TITLE OF INVENTION: ADRENERGIC RECEPTOR
;  FILE REFERENCE: PF128D2C1
;  CURRENT APPLICATION NUMBER: US/09/951,622
;  CURRENT FILING DATE: 2001-09-14
;  PRIOR APPLICATION NUMBER: 09/339,244
;  PRIOR FILING DATE: 1999-06-24
;  PRIOR APPLICATION NUMBER: 09/030,582
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 08/467,568
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: PCT/US94/09051
;  PRIOR FILING DATE: 1994-08-10
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 517
;   TYPE: PRT
;   ORGANISM: human
US-09-951-622-10

  Query Match             15.2%;  Score 319;  DB 10;  Length 517;
  Best Local Similarity   26.4%;  Pred. No. 2.8e-21;
  Matches   92;  Conservative   66;  Mismatches  160;  Indels   30;  Gaps    7;

Qy         14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
Db         32 SSNSTLP--QLDITRAISVGLVLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87

Qy         74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
Db         88 AMADLLLSFTVLPFSAALEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147

Qy        134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
Db        148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204

Qy        194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL------YNVKRHSLEVPVKDCVENE 245
Db        205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262

Qy        246 DEEGAEKKEEFQDEMNIPESLPPSPRPNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305
Db        263 DTLSSTKAKGHNPRSSIAVKLFKFSREK-----------KAAKTLGIVVGMFILCWLPF 310

Qy        306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKK 353
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Db     311 -FIALPLGSLFSTLKPPDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKR 357


RESULT 13
US-10-185-991-4
; Sequence 4, Application US/10185991
; Publication No. US20030022900A1
;   GENERAL INFORMATION:
;        APPLICANT: Charles Gluchowski, et al.
;        TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
;                            TREAT BENIGN PROSTATIC HYPERPLASIA
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: COOPER & DUNHAM LLP
;             STREET: 1185 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: U.S.A.
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.24
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/185,991
;             FILING DATE: 28-Jun-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/444,783
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: White, John P.
;             REGISTRATION NUMBER: 28,678
;             REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 278-0400
;             TELEFAX: (212) 391-0525
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 520 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-185-991-4

  Query Match             15.2%;  Score 319;  DB 9;  Length 520;
  Best Local Similarity   26.4%;  Pred. No. 2.8e-21;
  Matches   92;  Conservative   66;  Mismatches  160;  Indels   30;  Gaps    7;

Qy      14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
           ||:: :|     : :   |    ||  |:  : ||||:: | :     |   || || ||
Db      32 SSNSTLP----QLDITRAISVGLVLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87

Qy      74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
           : |||    | |:  |  |  :| |   ||     ::  |   ||: ::  :|:|||: :
Db      88 AMADLLLSFTVLPFSAALEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147

Qy     134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
           : | ||: :|:|:  | |  |::: : |  || || : | :: :  | :     | |
Db     148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204

Qy     194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL--------YNVKRHSLEVRVKDCVENE 245
           : | :    ||| |::  |  |:  |:|    |          | |  :| :  |:  :|
Db     205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262

Qy     246 DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305
           |   : | :      :|   |    |              |||| : |::  ::|    |:
Db     263 DTLSSTKAKGHNPRSSIAVKLFKFSREK-----------KAAKTLGIVVGMFILCWLPF 310

Qy     306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKK 353
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           |:|:    :    : |  |  :: || :   |::| :|    |  |:
Db     311 -FIALPLGSLFSTLKPPDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKR 357


RESULT 14
US-10-080-960-25
; Sequence 25, Application US/10080960
; Publication No. US20020197695A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Glucksmann, Maria
;  APPLICANT:  Meyers, Rachel
;  TITLE OF INVENTION: 80090, 52874,52880,63497, AND 33425
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
;  FILE REFERENCE: 38155-20044.00
;  CURRENT APPLICATION NUMBER: US/10/080,960
;  CURRENT FILING DATE:  2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/242,040
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/242,038
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/241,992
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/242,637
;  PRIOR FILING DATE: 2000-10-23
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 259
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus amino acid sequence
US-10-080-960-25

  Query Match             14.3%;  Score 299;  DB 9;  Length 259;
  Best Local Similarity   23.2%;  Pred. No. 7.7e-20;
  Matches   76;  Conservative   56;  Mismatches   97;  Indels   98;  Gaps    8;

Qy      48 GNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWVVATSV--PLFWPLNSHFCT 105
           ||::: ||: |  :|   || || || | ||| :  : || :   |     ||  |  |
Db       1 GNLLVILVILRTKKLRTPTNIFILNLAVADLLFLLTLPPWALYYLVGGSEDWPFGSALCK 60

Qy     106 ALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQ-RRGYLLLYGTWIVAILQST 164
           : :|  :  :||:  :  :|:|||:|:||| |  : |  ||  :::   |::|:| |
Db      61 LVTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLVWVLALLLSL 120

Qy     165 PP-LYGWGQAA----------------FDERNALCSMIWGASPSYTILSVVSFIVIPLI 206
           || |: | :                  | | :      |     || :|| :   ::||:
Db     121 PPLLFSWVKTVEEGNGTLNVNVTVCLIDFPEESTASVSTW--LRSYVLLSTLVGFLLPLL 178

Qy     207 VMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIPESL 266
           |:: ||: :    |
Db     179 VILVCYTRILRTLR---------------------------------------------- 192

Qy     267 PPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY---------CFLAVLAVWVDV 317
                             |||| : :::  :||   ||          |   :::   ::
Db     193 ------------------KAAKTLLVVVVVFVLCWLPYFIVLLLDTLCLSIIMSSTCEL 233

Qy     318 ETQVPQWVITIIIWLFFLQCCIHPYVY 344
           |  :|   : : :|| ::  |::| :|
Db     234 ERVLPT-ALLVTLWLAYVNSCLNPIIY 259


RESULT 15
US-10-012-140-27
; Sequence 27, Application US/10012140
; Publication No. US20030009017A1
; GENERAL INFORMATION:
;  APPLICANT: Leiby, Kevin R.
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Glucksmann, Maria A.
;  TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
```

; TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 38155-2004900
; CURRENT APPLICATION NUMBER: US/10/012,140
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 60/246,768
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,772
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,185
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-012-140-27

Query Match 14.3%; Score 299; DB 9; Length 259;
Best Local Similarity 23.2%; Pred. No. 7.7e-20;
Matches 76; Conservative 56; Mismatches 97; Indels 98; Gaps 8;

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Qy      48 GNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWVVATSV--PLFWPLNSHFCT 105
           ||:.. ||. |  .|   || || || | ||| .  . || :   |     ||  |  |
Db       1 GNLLVILVILRTKKLRTPTNIFILNLAVADLLFLLTLPPWALYYLVGGSEDWPFGSALCK 60

Qy     106 ALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQ-RPGYLLLYGTWIVAILQST 164
           : :|  .  .||       .| |||| |.||| |    |  ||  ..     |:.|:| |
Db      61 LVTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLVWVLALLLSL 120

Qy     165 PP-LYGWGQAA----------------FDERNALCSMIWGASPSYTILSVVSFIVIPLI 206
           || |: | :                  | | :      |    || .|| .   ..||.
Db     121 PPLLFSWVKTVEEGNGTLNVNVTVCLIDFPEESTASVSTW--LRSYVLLSTLVGFLLPLL 178

Qy     207 VMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIPESL 266
           |:: ||: :    |
Db     179 VILVCYTRILRTLR---------------------------------------------- 192

Qy     267 PPSRRNSNSNPPLPKCYQCKAAKVIFIIIFSYVLSLGPY---------CFLAVLAVWVDV 317
                           |||| : :::  .||   ||         |   .::   ..
Db     193 ------------------KAAKTLLVVVVVFVLCWLPYFIVLLLDTLCLSIIMSSTCEL 233

Qy     318 ETQVPQWVITIIIWLFFLQCCIHPYVY 344
           | .:|  . .  :|    ! .| .|
Db     234 ERVLPT-ALLVTLWLAYVNSCLNPIIY 259
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Search completed: February 11, 2003, 11:11:37
Job time : 15 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 11, 2003, 11:06:10 ; Search time 21 Seconds
(without alignments)
1821.976 Million cell updates/sec

Title: US-09-841-741-2
Perfect score: 2093
Sequence: 1 MTSTCTNSTRESNSSHTCMP.....GTEGGTEGKIVPSYDSATFP 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	371	17.7	466	2	I57959	alpha-1C adrenergi
2	366.5	17.5	429	2	S65656	alpha-1C-adrenergi
3	366.5	17.5	466	2	JN0765	alpha-1C-adrenergi
4	366.5	17.5	499	2	S65657	alpha-1C-adrenergi
5	356.5	17.0	466	2	A35375	alpha-1-adrenergic
6	354	16.9	477	2	S71323	alpha-1A adrenergi
7	331.5	15.8	422	2	JH0315	serotonin receptor
8	326.5	15.6	501	2	JH0447	alpha-1A-adrenergi
9	326.5	15.6	572	2	I39369	alpha-1A-adrenergi
10	324	15.5	515	2	JC1525	alpha-1B-adrenergi
11	321.5	15.4	422	2	I38209	serotonin receptor
12	320.5	15.3	421	2	I49375	serotonin receptor
13	319	15.2	515	2	A40491	alpha-1-adrenergic
14	319	15.2	517	2	A45121	alpha-1B adrenergi
15	314.5	15.0	560	2	A38731	alpha-1A adrenergi
16	305	14.6	509	2	A47174	serotonin receptor
17	299	14.3	448	2	A47519	serotonin receptor
18	297	14.2	445	2	A48881	serotonin receptor
19	296.5	14.2	490	2	A35546	muscarinic acetylc
20	296	14.1	448	2	S36402	serotonin receptor
21	285	13.6	443	1	DYHUD2	dopamine receptor
22	284	13.6	318	2	S38511	adenosine receptor
23	280.5	13.4	484	2	S48657	muscarinic acetylc
24	277.5	13.3	459	2	A43951	serotonin receptor
25	277	13.2	458	2	JS0616	serotonin receptor
26	276	13.2	430	2	T16079	hypothetical prote
27	276	13.2	564	2	A38271	serotonin receptor
28	275	13.1	460	2	A32605	serotonin receptor
29	274.5	13.1	400	2	S32804	beta-3-adrenergic
30	273.5	13.1	444	1	DYBOD2	dopamine receptor
31	273	13.0	479	2	S33776	muscarinic acetylc
32	272.5	13.0	415	2	I53040	beta-2 adrenergic
33	271.5	13.0	478	2	C29514	muscarinic acetylc
34	271	12.9	444	1	DYMSD2	dopamine receptor
35	271	12.9	444	1	S08146	dopamine receptor
36	271	12.9	466	2	S36794	beta-1-adrenergic
37	270	12.9	488	2	T15941	hypothetical prote
38	269	12.9	477	1	QRHUB1	beta-1-adrenergic
39	269	12.9	479	2	S10127	muscarinic acetylc
40	268.5	12.8	400	2	A53281	beta 3-adrenergic
41	268.5	12.8	471	2	A43956	serotonin receptor
42	267.5	12.8	413	1	QRHUB2	beta-2-adrenergic
43	266.5	12.7	446	1	DYHUD1	dopamine receptor
44	266	12.7	363	2	I50475	dopamine D1 recept
45	265.5	12.7	420	2	I51666	Mel-1c receptor su

ALIGNMENTS

RESULT 1
I57959
alpha-1C adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Apr-2000
C;Accession: I57959; I52862; PC2179
R;Laz, T.M.; Forray, C.; Smith, K.E.; Bard, J.A.; Vaysse, P.J.; Branchek, T.A.; Weinshank
Mol. Pharmacol. 46, 414-422, 1994
A;Title: The rat homologue of the bovine alpha 1c-adrenergic receptor shows the pharmacol
A;Reference number: I57959; MUID:95021119; PMID:7935320
A;Accession: I57959
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-466 <RES>
A;Cross-references: EMBL:U07126; NID:g595275; PIDN:AAA62866.1; PID:g595276
R;Stewart, A.F.; Rokosh, D.G.; Bailey, B.A.; Karns, L.R.; Chang, K.C.; Long, C.S.; Kariya
Circ. Res. 75, 796-802, 1994
A;Title: Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. alpha 1C,
A;Reference number: I52862; MUID:95008062; PMID:7923624
A;Accession: I52862
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-38,'L',40-66,'G',68-466 <RE2>
A;Cross-references: EMBL:U13368; NID:g555851; PIDN:AAA52103.1; PID:g555852
R;Rokosh, D.G.; Bailey, B.A.; Stewart, A.F.R.; Karns, L.R.; Long, C.S.; Simpson, P.C.
Biochem. Biophys. Res. Commun. 200, 1177-1184, 1994
A;Title: Distribution of alpha 1C-adrenergic receptor mRNA in adult rat tissues by RNase
A;Reference number: PC2179; MUID:94241969; PMID:8185565
A;Accession: PC2179
A;Molecule type: mRNA
A;Residues: 102-279 <ROK>
A;Experimental source: cardiac myocyte
C;Comment: This factor comprises a multigene family. As do alpha-2 and beta-adrenergic re
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor; transmembrane protein
F;26-42/Domain: transmembrane #status predicted <TM1>
F;73-89/Domain: transmembrane #status predicted <TM2>
F;104-120/Domain: transmembrane #status predicted <TM3>
F;147-163/Domain: transmembrane #status predicted <TM4>
F;195-211/Domain: transmembrane #status predicted <TM5>
F;276-292/Domain: transmembrane #status predicted <TM6>
F;306-329/Domain: transmembrane #status predicted <TM7>

Query Match 17.7%; Score 371; DB 2; Length 466;
Best Local Similarity 26.1%; Pred. No. 1.3e-23;
Matches 106; Conservative 78; Mismatches 180; Indels 42; Gaps 10;

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Qy       7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
           |::  || :|        |:::  |:   :|   :   :|||:: | :     |  ||
Db       7 NASEGSNCTH-----PPAPVNISKAILLGVILGGLIIFGVLGNILVILSVACHRHLHSVT 61

Qy      67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
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Db     62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIIS 121

Qy    127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186

Db    122 IDRYIGVSYPLRYPTIVTQRRGVRALLCVWVLSLVISIGPLFGWRQPA-PEDETICQI-- 178

Qy    187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242

Db    179 NEEPGYVLFSALGSFYVPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLPIHP 238

Qy    243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297

Db    239 KNVPAEGGGVSSAKNKTHFSVRL-----LKFSREK------------KAAKTLGIVVGC 280

Qy    298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357

Db    281 FVLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy    358 MLKFFCKEKPPKEDS     HPDLPGTEGGTEGKI VPSYDSATF 397

Db    340 VLRIQCLRPPQSSKHALGYTLHPPSQALEGQHRDMVRIPVGSGETF 385


RESULT 2
S65656
alpha-1C-adrenergic receptor splice form 3 - human
N;Alternate names: alpha-1C-adrenoceptor isoform 3
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Jun-2000
C;Accession: S65656; S65654
R;Tanaka, T.
submitted to the EMBL Data Library, July 1994
A;Reference number: S65656
A;Accession: S65656
A;Molecule type: mRNA
A;Residues: 1-429 <TAN>
A;Cross-references: EMBL:D32201, NID.g927210; PIDN.BAA06900.1, PID.g927211
R;Hirasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;
FEBS Lett. 363, 256-260, 1995
A;Title: Cloning, functional expression and tissue distribution of human alpha(1C)-adren
A;Reference number: S65654; MUID:95255557; PMID:7737411
A;Accession: S65654
A;Molecule type: mRNA
A;Residues: 424-429 <HIR>
A;Cross-references: EMBL:D32201
C;Genetics:
A;Gene: GDB:ADRA1C; ADRA1L1
A;Cross-references: GDB:128088; OMIM:104221
A;Map position: 8p21 8p11.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; neurotransmitter receptor

  Query Match             17.5%;  Score 366.5;  DB 2;  Length 429;
  Best Local Similarity   26.7%;  Pred. No. 2.8e-23;
  Matches  108;  Conservative   76;  Mismatches  182;  Indels   39;  Gaps   10;

Qy      8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67

Db      5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy     68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127

Db     63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy    128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187

Db    123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy    188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243

Db    180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESPGLKSGLKTDKSDSEQVTLRIHRK 239

Qy    244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298

Db    240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy    299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358

Db    282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy    359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397

Db    341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385


RESULT 3
JN0765
alpha-1C-adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul 2000
C;Accession: JN0765; I84635; JC2333; G01419
R;Hirasawa, A.; Horie, K.; Tanaka, T.; Takagaki, K.; Murai, M.; Yano, J.; Tsujimoto, G.
Biochem. Biophys. Res. Commun. 195, 902-909, 1993
A;Title: Cloning, functional expression and tissue distribution of human cDNA for the alp
A;Reference number: JN0765; MUID:93384619; PMID:8396931
A;Accession: JN0765
A;Molecule type: mRNA
A;Residues: 1-466 <HIR>
A;Cross-references: GB:L31774; NID:g666892; PIDN:AAB59486.1; PID:g666893
R;Diehl, N.L.; Shreeve, S.M.
Eur. J. Pharmacol. 268, 393-398, 1994
A;Title: Identification of the alpha 1c adrenoceptor in rabbit arteries and the human sap
A;Reference number: I47013; MUID:95104335; PMID:7805763
A;Accession: I84635
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 202-344 <DIE>
A;Cross-references: GB:S76001; NID:g913817; PIDN:AAD14205.1; PID:g4261905
R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.; S
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors alp
A;Reference number: JC2331; MUID:94296402; PMID:8024574
A;Accession: JC2333
A;Molecule type: mRNA
A;Residues: 1-130,'F',132-140,'P',142-166,'C',168-247,'H',249-337,'C',339-430,'Q',432-466
A;Cross-references: GB:S70782; NID:g547219; PIDN:AAB31163.1; PID:g547220
R;Elliston, K.O.
submitted to the EMBL Data Library, April 1994
A;Reference number: G06938
A;Accession: G01419
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 296-346,'C',348-430,'Q',432-466 <ELL>
A;Cross-references: EMBL:U08994; NID:g497243; PIDN:AAA18783.1; PID:g497244
C;Comment: This protein plays critical roles in the regulation of a variety of physiolog
C;Genetics.
A;Gene: GDB:ADRA1C; ADRA1L1
A;Cross-references: GDB:128088; OMIM:104221
A;Map position: 8p21-8p11.2
A;Introns: 295/3
A;Note: the list of introns may be incomplete
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; glycoprotein; receptor; transmembrane protein
F;26-51/Domain: transmembrane #status predicted <TM1>
F;66-90/Domain: transmembrane #status predicted <TM2>
F;101-122/Domain: transmembrane #status predicted <TM3>
F;144-165/Domain: transmembrane #status predicted <TM4>
F;183-205/Domain: transmembrane #status predicted <TM5>
F;274-298/Domain: transmembrane #status predicted <TM6>
F;306-329/Domain: transmembrane #status predicted <TM7>
F;7,13,22/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             17.5%;  Score 366.5;  DB 2;  Length 466;
  Best Local Similarity   26.7%;  Pred. No. 3.1e-23;
  Matches  108;  Conservative   76;  Mismatches  182;  Indels   39;  Gaps   10;
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Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385
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RESULT 4
S65657
alpha-1C-adrenergic receptor splice form 2 - human
N;Alternate names: alpha-1C-adrenoceptor isoform 2
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Jun-2000
C;Accession: S65657; S65655
R;Tanaka, T.
submitted to the EMBL Data Library, July 1994
A;Reference number: S65656
A;Accession: S65657
A;Molecule type: mRNA
A;Residues: 1-499 <TAN>
A;Cross-references: EMBL:D32202; NID:g927208; PIDN:BAA06901.1; PID:g927209
R;Hirasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;
FEBS Lett. 363, 256-260, 1995
A;Title: Cloning, functional expression and tissue distribution of human alpha(1C)-adrer
A;Reference number: S65654; MUID:95255557; PMID:7737411
A;Accession: S65655
A;Molecule type: mRNA
A;Residues: 424-499 <HIR>
A;Cross-references: EMBL:D32202
C;Genetics:
A;Gene: GDB:ADRA1C; ADRA1L1
A;Cross-references: GDB:128088; OMIM:104221
A;Map position: 8p21-8p11.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; neurotransmitter receptor

  Query Match   17.5%; Score 366.5; DB 2; Length 499;
  Best Local Similarity 26.7%; Pred. No. 3.3e-23;
  Matches 108; Conservative   76; Mismatches 182; Indels   39; Gaps   10;

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Qy       8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
Db       5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62

Qy      68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
Db      63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122

Qy     128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
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Db     123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179

Qy     188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
Db     180 EEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239

Qy     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
Db     240 NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------------KAAKTLGIVVGCF 281

Qy     299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
Db     282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340

Qy     359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
Db     341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385
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RESULT 5
A35375
alpha-1-adrenergic receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A35375
R;Schwinn, D.A.; Lomasney, J.W.; Lorenz, W.; Szklut, P.J.; Fremeau Jr., R.T.; Yang-Feng,
J. Biol. Chem. 265, 8183-8189, 1990
A;Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic rece
A;Reference number: A35375; MUID:90243698; PMID:1970822
A;Accession: A35375
A;Molecule type: mRNA
A;Residues: 1-466 <SCH>
A;Cross-references: GB:J05426; NID:g162663; PIDN:AAA30374.1; PID:g162664
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote

  Query Match   17.0%; Score 356.5; DB 2; Length 466;
  Best Local Similarity 25.5%; Pred. No. 2.1e-22;
  Matches 108; Conservative   74; Mismatches 176; Indels   65; Gaps   10;

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Qy       7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
Db       7 NASDSSNCTH-----PPPPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT 61

Qy      67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
Db      62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNVWAAVDVLCCTASIMGLCIIS 121

Qy     127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
Db     122 IDPYIGVSYPLRYPTIVTQKRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI-- 178

Qy     187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
Db     179 NEEPGYVLFSALGSFYVPLTIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHR 238

Qy     243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
Db     239 KNAQVGGSGVTSAKNKTHFSVRL-----LKFSREK------------KAAKTLGIVVGC 280

Qy     298 YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
Db     281 FVLCWLPF-FLVMPIGSFFPDFRPSETVFKIAFWLGYLNSCINPIIYPCSSQEFKKAFQN 339

Qy     358 MLKKFFCKEKPPK--------------EDSHPDL-------------PGTEGGTEGKI 388
Db     340 VLRIQCLRRKQSSKHTLGYTLHAPSHVLEGQHKDLVRIPVGSAETFYKISKTDGVCEWKI 399

Qy     389 VPS 391
Db     400 FSS 402
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```
RESULT 6
S71323
alpha-1A adrenergic receptor - Japanese medaka
C;Species: Oryzias latipes (Japanese medaka)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C;Accession: S71323
R;Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996
A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me
A;Reference number: S71323; MUID:96184522; PMID:8654394
A;Accession: S71323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <YAS>
A;Cross-references: EMBL:D63859
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
C;Superfamily: vertebrate rhodopsin

  Query Match             16.9%;  Score 354;  DB 2;  Length 477;
  Best Local Similarity   28.0%;  Pred. No. 3.6e-22;
  Matches  109;  Conservative   63;  Mismatches  193;  Indels   24;  Gaps   10;

Qy      12 SNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQPKPQLLQVTNPFIF 71
Db      18 SNCSHVLAP----ELNTVKAVVLGMVLGIFILFGVIGNILVILSVVCHRHLQTVTYYFIV 73

Qy      72 NLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYL 131
Db      74 NLAVADLLLSSTVLPFSAIFEILDPWVFGRVFCNIWAAVDVLCCTASIMSLCVISVDRYI 133

Qy     132 SIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPS 191
Db     134 GVSYPLRYPAIMTKRRALLAVMLLWVLSVIISIGPLFGWKEPA-PEDETVCKIT--EEPG 190

Qy     192 YTILSVVSFIVIPLIVMIACYSVVFCAAPPQHALLYNVKRHSLEVRVKDCVENEDEEGAE 251
Db     191 YAIFSAVGSFYLPLAIILAMYCRVYVVAQKE----------SRGLKEGQKIEKSDSEQVI 240

Qy     252 KKEEFQDEMNIPESLPPSPPNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVL 311
Db     241 LRMH-RGNTTVSEDEALRSRTHFALRLLKFSREKKAAKTLGIVVGCFVLCWLP--FFLVL 297

Qy     312 AVWVDVETQVP-QWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
Db     298 PIGSIFPAYRPSDTVFKITFWLGYFNSCINPIIYLCSNQEFKKAFQSLL-GVHCLRMTPR 356

Qy     371 EDSHPDLPGTEGGTEG-KIVPSYDSATFP 398
Db     357 AHHH-HLSVGQSQTQGHSLTISLDSKGAP 384

RESULT 7
JH0315
serotonin receptor 1A - rat
N;Alternate names: 5-hydroxytryptamine receptor 1A (5-HTR1A)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Aug-1999
C;Accession: JH0315; A35181
R;Fujiwara, Y.; Nelson, D.L.; Kashihara, K.; Varga, E.; Roeske, W.R.; Yamamura, H.I.
Life Sci. 47, 127-132, 1990
A;Title: The cloning and sequence analysis of the rat serotonin-1A receptor gene.
A;Reference number: JH0315; MUID:90355775; PMID:2167416
A;Accession: JH0315
A;Molecule type: DNA
A;Residues: 1-422 <FUJ>
R;Albert, P.R.; Zhou, Q.Y.; Van Tol, H.H.M.; Bunzow, J.R.; Civelli, O.
J. Biol. Chem. 265, 5825-5832, 1990
A;Title: Cloning, functional expression, and mRNA tissue distribution of the rat 5-hydro
A;Reference number: A35181; MUID:90202832; PMID:2156831
A;Accession: A35181
A;Molecule type: DNA
A;Residues: 1-372,'S',374-422 <ALB>
A;Cross-references: GB:J05276; NID:g202540; PIDN:AAA40612.1; PID:g202541
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
F;37-62/Domain: transmembrane #status predicted <TM1>
F;74-98/Domain: transmembrane #status predicted <TM2>
F;109-134/Domain: transmembrane #status predicted <TM3>
F;153-178/Domain: transmembrane #status predicted <TM4>
F;252-277/Domain: transmembrane #status predicted <TM5>
F;346-371/Domain: transmembrane #status predicted <TM6>
F;379-404/Domain: transmembrane #status predicted <TM7>

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  Best Local Similarity   24.4%;  Pred. No. 2.5e-20;
  Matches   98;  Conservative   69;  Mismatches  163;  Indels   71;  Gaps    8;

Qy      26 ISLAHGIIRSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 83
Db      31 VTFSYQVITSLLLGTLIFCAVLGNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88

Qy      84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
Db      89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148

Qy     144 TQPRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
Db     149 TPRRAAALISLTWLIGFLISIPPMLGWRTP--EDPSDPDACTISKDHGYTIYSTFGAFYI 206

Qy     204 PLIVMIACYSVVFCAARPQHALLYNVKRHSLEVRVKD------------------------ 240
Db     207 PLLLMLVLYGRIFRAAR------FRIRKTVPKVEKKGAGTSLGTSSAPPPKKSLNGQPGS 260

Qy     241 ----CVENE----------DEEGAEKKEEFQDEMNIPESLP PSPPNSNSNPP-- 278
Db     261 GDWRRCAENRAVGTPCTNGAVRQGDDEATLEVIEVHRVGNSKEHLPLPSESGSNSYAPAC 320

Qy     279 -------------LPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQW 324
Db     321 LERKNERNAEAKRKMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCENSCHMPAL 380

Qy     325 VITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCK 365
Db     381 LGAIINWLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCKFCR 421

RESULT 8
JH0447
alpha-1A-adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
C;Accession: JH0447
R;Bruno, J.F.; Whittaker, J.; Song, J.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 179, 1485-1490, 1991
A;Title: Molecular cloning and sequencing of a cDNA encoding a human alpha 1A adrenergic
A;Reference number: JH0447; MUID:92028892; PMID:1656955
A;Accession: JH0447
A;Molecule type: mRNA
A;Residues: 1-501 <BRU>
A;Cross-references: GB:M76446; NID:g177806; PIDN:AAA35496.1; PID:g177807
A;Experimental source: hippocampus
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;56-79/Domain: transmembrane #status predicted <TM1>
F;93-116/Domain: transmembrane #status predicted <TM2>
F;128-151/Domain: transmembrane #status predicted <TM3>
F;172-196/Domain: transmembrane #status predicted <TM4>
F;210-233/Domain: transmembrane #status predicted <TM5>
F;308-331/Domain: transmembrane #status predicted <TM6>
F;339-363/Domain: transmembrane #status predicted <TM7>

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  Best Local Similarity   27.7%;  Pred. No. 8e-20;
  Matches   96;  Conservative   58;  Mismatches  157;  Indels   35;  Gaps   10;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
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Db      52 AQGVGVGVFLAAFILMAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLPFS 111

Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148

Db     112 ATMEVLGFWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 171

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207

Db     172 AAILALLWVVALVVSVGPLLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLPMAV 227

Qy     208 MIACYSVVFCAAR-RQHALLYNVKRHS-------LEVRVKDCVENEDEEGAE-----KKE 254

Db     228 IVVMYCRVYVVARSTTRSLEAGVKRERGKASEVVLRIHCRGAATGAD--GAHGMRSAKGH 285

Qy     255 EFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVW 314

Db     286 TFRSSLSV-RLLKFSREK------------KAAKTLAIVVGVFVLCWFPFFFVLPLGS- 330

Qy     315 VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360

Db     331 LFPQLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 376


RESULT 9
I39369
alpha-1A-adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 13-Aug-1999
C;Accession: I39369; JC2331
R;Esbenshade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Minneman, K.P.; M
Mol. Pharmacol. 47, 977-985, 1995
A;Title: Cloning of the human alpha 1d-adrenergic receptor and inducible expression of t
A;Reference number: I39369; MUID:95265059; PMID:7746284
A;Accession: I39369
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <RES>
A;Cross-references: GB:D29952; NID:g914933; PIDN:BAA06222.1; PID:g914934
R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors al
A;Reference number: JC2331; MUID:94296402; PMID:8024574
A;Accession: JC2331
A;Molecule type: mRNA
A;Residues: 1-30,'G',32-521,'P',523-572 <WEI>
A;Note: the authors translated the codon CCC for residue 522 as Arg
C;Genetics:
A;Gene: GDB:ADRA1A; ADRA1; ADRA1R
A;Cross-references: GDB:118749; OMIM:104219
A;Map position: 20pter-20qter
A;Introns: 37/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;89-123/Domain: transmembrane #status predicted <TM1>
F;132-162/Domain: transmembrane #status predicted <TM2>
F;172-197/Domain: transmembrane #status predicted <TM3>
F;208-235/Domain: transmembrane #status predicted <TM4>
F;254-278/Domain: transmembrane #status predicted <TM5>
F;344-374/Domain: transmembrane #status predicted <TM6>
F;380-414/Domain: transmembrane #status predicted <TM7>
F;65,82/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           15.6%;  Score 326.5;  DB 2;  Length 572;
  Best Local Similarity   27.7%;  Pred. No. 9.3e-20;
  Matches   96;  Conservative   58;  Mismatches  157;  Indels   35;  Gaps   10;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88

Db      94 AQGVGVGVFLAAFILMAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLPFS 153

Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148

Db     154 ATMEVLGFWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 213

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207

Db     214 AAILALLWVVALVVSVGPLLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLPMAV 269

Qy     208 MIACYSVVFCAAR-RQHALLYNVKRHS-------LEVRVKDCVENEDEEGAE-----KKE 254

Db     270 IVVMYCRVYVVARSTTRSLEAGVKRERGKASEVVLRIHCRGAATGAD--GAHGMRSAKGH 327

Qy     255 EFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVW 314

Db     328 TFRSSLSV-RLLKFSREK------------KAAKTLAIVVGVFVLCWFPFFFVLPLGS- 372

Qy     315 VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360

Db     373 LFPQLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 418


RESULT 10
JC1525
alpha-1B-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
C;Accession: JC1525; S08400
R;Gao, B.; Kunos, G.
Gene 131, 243-247, 1993
A;Title: Isolation and characterization of the gene encoding the rat alpha 1B adrengergic
A;Reference number: JC1525; MUID:94010315; PMID:8406017
A;Accession: JC1525
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-515 <GAO>
A;Cross-references: GB:L08610; NID:g202624; PIDN:AAA40647.1; PID:g202626
R;Voigt, M.M.; Kispert, J.; Chin, H.
Nucleic Acids Res. 18, 1053, 1990
A;Title: Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor.
A;Reference number: S08400; MUID:90192094; PMID:2156222
A;Accession: S08400
A;Molecule type: mRNA
A;Residues: 1-202,'C',204-206,'C',208-305,'C',307-414,'QK',417-439,'C',441-483,'ATA',487-
A;Cross-references: EMBL:X51585; NID:g55557; PIDN:CAA35934.1; PID:g55558
C;Genetics:
A;Introns: 317/1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match           15.5%;  Score 324;  DB 2;  Length 515;
  Best Local Similarity   26.3%;  Pred. No. 1.3e-19;
  Matches   93;  Conservative   70;  Mismatches  161;  Indels   30;  Gaps    7;

Qy      14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73

Db      32 SSNSTLPQLDVTRAISVGL----VLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87

Qy      74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133

Db      88 AIADLLLSFTVLPFSATLEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147

Qy     134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193

Db     148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204

Qy     194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL--------YNVKRHSLEVRVKDCVENE 245

Db     205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262

Qy     246 DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305

Db     263 DTLSSTKAKGHNPRSSIAVKLFKFSREK------------KAAKTLGIVVGMFILSWLPF 310

Qy     306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDML 359
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Db    311 -FIALPLGSLFSTLKPPDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKRAFMRIL 363

RESULT 11
I38209
serotonin receptor 1A - human
N;Alternate names: 5-hydroxytryptamine receptor 1A (5-HTR1A)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 15 May-1998 #text_change 21-Jul-2000
C;Accession: I38209; I37104; S07343; I56176; S31438
R;Jacobsen, J.S.; Refolo, L.M.; Conley, M.P.; Sambamurti, K.; Humayun, M.Z.
Mutat. Res. 179, 89-101, 1987
A;Title: DNA replication-blocking properties of adducts formed by aflatoxin B1-2,3-dichl
A;Reference number: I38209; MUID:87258013; PMID:3110609
A;Accession: I38209
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <JAC>
A;Cross-references: EMBL:X57829; NID:g36428; PIDN:CAA40962.1; PID:g36429
R;Parks, C.L.; Chang, L.S.; Shenk, T.
Nucleic Acids Res. 19, 7155-7160, 1991
A;Title: A polymerase chain reaction mediated by a single primer: cloning of genomic seq
A;Reference number: I37104; MUID:92115564; PMID:1766875
A;Accession: I37104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-9 <PAR>
A;Cross-references: EMBL:Z11168; NID:g1033027; PIDN:CAA77560.1; PID:g1033028
R;Kobilka, B.K.; Frielle, T.; Collins, S.; Yang-Feng, T.; Kobilka, T.S.; Francke, U.; Le
Nature 329, 75-79, 1987
A;Title: An intronless gene encoding a potential member of the family of receptors coupl
A;Reference number: S07343; MUID:87315369; PMID:3041227
A;Accession: S07343
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151,'PR',155-171,'I',173-417,'N',419-422 <KOB>
A;Cross-references: EMBL:X13556; NID:g35523; PIDN:CAA31908.1; PID:g35524
A;Note: the authors translated the codon ATC for residue 172 as Met
R;Aune, T.M.; McGrath, K.M.; Sarr, T.; Bombara, M.P.; Kelley, K.A.
J. Immunol. 151, 1175-1183, 1993
A;Title: Expression of 5HT1a receptors on activated human T cells. Regulation of cyclic
A;Reference number: I56176; MUID:93329096; PMID:8393041
A;Accession: I56176
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PPR',203-227,'R',229-244,'A',245-354,'T',356-362,'MRP' <AUN>
A;Cross-references: GB:S64045; NID:g404416; PIDN:AAD13945.1; PID:g4261645
C;Genetics:
A;Gene: GDB:HTR1A; ADRB2RL1; ADRBRL1
A;Cross-references: GDB:120686; OMIM:109760
A;Map position: 5cen-5q11
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter rece
F;37-62/Domain: transmembrane #status predicted <TM1>
F;74-98/Domain: transmembrane #status predicted <TM2>
F;110-132/Domain: transmembrane #status predicted <TM3>
F;153-178/Domain: transmembrane #status predicted <TM4>
F;192-217/Domain: transmembrane #status predicted <TM5>
F;346-367/Domain: transmembrane #status predicted <TM6>
F;379-403/Domain: transmembrane #status predicted <TM7>
F;10,11,24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;109-187/Disulfide bonds: #status predicted
F;420/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             15.4%;  Score 321.5;  DB 2;  Length 422;
  Best Local Similarity   24.0%;  Pred. No. 1.7e-19;
  Matches   95;  Conservative   72;  Mismatches  170;  Indels   59;  Gaps    7;

Qy     26 ISLAHGIIRSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 83
Db     31 VTVSYQVITSLLLGTLIFCAVLGNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88

Qy     84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
Db     89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148

Qy    144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
Db    149 TPRRAAALISLTWLIGFLISIPPMLGWRTP--EDRSDPDACTISKDHGYTIYSTFGAFYI 206

Qy    204 PLIVMIACYSVVFCAAR-RQHALLYNVKFHSLFVR------ --   -- ------     237
Db    207 PLLLMLVLYGRIFRAARFRIRKTVKKVEKTGADTRHGASPAPQPKKSVNGESGSRNWRLG 266

Qy    238 ----------VKDCVENEDEEGAEKKEEFQDEMNIPESLP-PS----------------R 270
Db    267 VESKAGGALCANGAVRQGDDGAALEVIEVHRVGNSKEHLPLPSEAGPTPCAPASFERKNE 326

Qy    271 RNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIII 330
Db    327 RNAEAKRKMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCESSCHMPTLLGAIIN 386

Qy    331 WLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKE 366
Db    387 WLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCKFCRQ 422

RESULT 12
I49375
serotonin receptor 1A - mouse
N;Alternate names: 5-hydroxytryptamine receptor 1A (5-HTR1A)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49375; A57508
R;Charest, A.; Wainer, B.H.; Albert, P.R.
J. Neurosci. 13, 5164-5171, 1993
A;Title: Cloning and differentiation-induced expression of a murine serotonin1A receptor
A;Reference number: I49375; MUID:94076019; PMID:8254366
A;Accession: I49375
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-421 <CHA>
A;Cross-references: EMBL:U39391; NID:g1066325; PIDN:AAA81519.1; PID:g1066326
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
Genomics 18, 175-184, 1993
A;Title: Identification, chromosomal location, and genome organization of mammalian G-pro
A;Reference number: A48909; MUID:94116290; PMID:8288218
A;Accession: A57508
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 136-176,'T',178-241,'L',243-246,'V',248-262,'W',264-303,'H',305-329,'I',331-3
A;Cross-references: GB:L20339
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
F;37-62/Domain: transmembrane #status predicted <TM1>
F;74-98/Domain: transmembrane #status predicted <TM2>
F;110-132/Domain: transmembrane #status predicted <TM3>
F;153-178/Domain: transmembrane #status predicted <TM4>
F;192-217/Domain: transmembrane #status predicted <TM5>
F;346-367/Domain: transmembrane #status predicted <TM6>
F;379-403/Domain: transmembrane #status predicted <TM7>
F;10,11,24,30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;109-187/Disulfide bonds: #status predicted

  Query Match             15.3%;  Score 320.5;  DB 2;  Length 421;
  Best Local Similarity   24.3%;  Pred. No. 2.1e-19;
  Matches   98;  Conservative   74;  Mismatches  155;  Indels   77;  Gaps   12;

Qy     26 ISLAHGIIRSTVLVIFLAASFVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL 83
Db     31 VTFSYQVITSLLLGTLIFCAVLGNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88

Qy     84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
Db     89 VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148
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Qy     144 TQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA-LCSMIWGASPSYTILSVVSFIV 202
Db     149 TPRRAAALISLTWLIGFLISIPPMLGW-RAPEDRSNPNECTI--SKDHGYTIYSTFGAFY 205

Qy     203 IPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVK---------------------- 239
Db     206 IPLLLMLVLYGRIFRAAR------FRIRKTVKKVEKKGAGTSFGTSSAPPPKKSLNGQPG 259

Qy     240 --DCVENEDE--------EGAEKKEEFQDEMNIPE---------SLP-PSRRNSNSNPPL 279
Db     260 SGDCRRSAENRAVGTPCANGAVRQGEDDATLEVIEVHRVGNSKGDLPLPSESGATSY--V 317

Qy     280 PRCY------------------QCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQV 321
Db     318 PACLERKNERTAEAKRKMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCESSCHM 377

Qy     322 PQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCK 365
Db     378 PELLGAIINWLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCKFCR 421
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RESULT 13
A40491
alpha-1-adrenergic receptor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A40491
R;Cotecchia, S.; Schwinn, D.A.; Randall, R.R.; Lefkowitz, R.J.; Caron, M.G.; Kobilka, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988
A;Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic
A;Reference number: A40491; MUID:89017157; PMID:2845398
A;Accession: A40491
A;Molecule type: mRNA
A;Residues: 1-515 <COT>
A;Cross-references: GB:J04084; NID:g619407; PIDN:AAA58964.1; PID:g619408
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

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Matches 92; Conservative 70; Mismatches 162; Indels 30; Gaps 7;

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Db      32 SSNSTLPQLDVTRAISVGL----VLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87

Qy      74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
Db      88 AIADLLLSFTVLPFSATLEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147

Qy     134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
Db     148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204

Qy     194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL--------YNVKRHSLEVRVKDCVENE 245
Db     205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262

Qy     246 DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305
Db     263 DTLSSTKAKGHNPRSSIAVKLFKFSREK-----------KAAKTLGIVVGMFILCWLPF 310

Qy     306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDML 359
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RESULT 14
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alpha-1B adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Apr-2000
C;Accession: A45121; JC2332
R;Ramarao, C.S.; Denker, J.M.; Perez, D.M.; Gaivin, R.J.; Riek, R.P.; Graham, R.M.
J. Biol. Chem. 267, 21936-21945, 1992
A;Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor.
A;Reference number: A45121; MUID:93016158; PMID:1328250
A;Accession: A45121
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-517 <RAM>
A;Cross-references: GB:M99590; NID:g178211
A;Note: sequence extracted from NCBI backbone (NCBIP:116785)
A;Note: this translation is not annotated in GenBank entry HUMADRENB, release 113.0 #date
R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.; S
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors alp
A;Reference number: JC2331; MUID:94296402; PMID:8024574
A;Accession: JC2332
A;Molecule type: mRNA
A;Residues: 1-158,'P',160-244,'H',246-314,'F',316-380,382-517 <WEI>
C;Genetics:
A;Gene: GDB:ADRA1B
A;Cross-references: GDB:127901; OMIM:104220
A;Map position: 5q31.1-5q33.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;39-72/Domain: transmembrane #status predicted <TM1>
F;81-111/Domain: transmembrane #status predicted <TM2>
F;121-146/Domain: transmembrane #status predicted <TM3>
F;157-184/Domain: transmembrane #status predicted <TM4>
F;203-227/Domain: transmembrane #status predicted <TM5>
F;290-320/Domain: transmembrane #status predicted <TM6>
F;326-360/Domain: transmembrane #status predicted <TM7>

Query Match 15.2%; Score 319; DB 2; Length 517;
Best Local Similarity 26.4%; Pred. No. 3.6e-19;
Matches 92; Conservative 66; Mismatches 160; Indels 30; Gaps 7;

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Db      32 SSNSTLP----QLDITRAISVGLVLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87

Qy      74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
Db      88 AMADLLLSFTVLPFSAALEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147

Qy     134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
Db     148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204

Qy     194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL--------YNVKRHSLEVRVKDCVENE 245
Db     205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262

Qy     246 DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305
Db     263 DTLSSTKAKGHNPRSSIAVKLFKFSREK-----------KAAKTLGIVVGMFILCWLPF 310

Qy     306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKK 353
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RESULT 15
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alpha-1A adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Apr-2000
C;Accession: A38731; A53280
R;Lomasney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.;
J. Biol. Chem. 266, 6365-6369, 1991
A;Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic recepto
A;Reference number: A38731; MUID:91177889; PMID:1706716
A;Accession: A38731
A;Molecule type: mRNA

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A;Residues: 1-560 <LOM>
A;Cross-references: GB:M60654; NID:g202761; PIDN:AAA63477.1; PID:g202762
R;Perez, D M ; Piascik, M T.; Graham, R M
Mol. Pharmacol. 40, 876-883, 1991
A;Title: Solution-phase library screening for the identification of rare clones: isolati
A;Reference number: A53280; MUID:92100054; PMID:1661838
A;Accession: A53280
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-36,'D',38-58,'I',60-202,'I',204-305,'R',307-366,'I',368-370,'I',372-559 <P
A;Experimental source: hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:73541)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein coupled receptor; glycoprotein; transmembrane protein

  Query Match             15.0%;  Score 314.5;  DB 2;  Length 560;
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  Matches   94;  Conservative   59;  Mismatches  162;  Indels   27;  Gaps    8;

Qy      29 AHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
           | |.     |  |       ||  |        |  ||| || || | |||    | |
Db      88 AQGVGVGVFLAAFILTAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSAAVLPFS 147

Qy      89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
             |  ||     ||    :   |   ||  :    ||||     | | ||  ||:|:
Db     148 ATMEVLGFWAFGRTFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 207

Qy     149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207
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Db     208 AAIIAILWAVALVVSVGPLLGWKEPVPPDER--FCGIT--EEVGYAIFSSVCSFYLPMAV 263

Qy     208 MIACYSVVFCAARFQHALLYNVKRHSLEVPVKDCVENEDEEGAE  KKEEFQDEMNIPES 265
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Db     264 IVVMYCPVYVVARS--------TTPSLEAGIK----REPGKASEVVLRIHCRGAATSAKG 311

Qy     266 LFPSR -     FNSNSNPPLPFCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVE 318
             | ::       | | |   |      |||   |:    ||   |: |   |      :
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Qy     319 TQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
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